

Remarks

In view of the above amendments and the following remarks, reconsideration of the outstanding office action is respectfully requested.

Claim 1 has been amended, claims 3-5 have been cancelled without prejudice, and new claims 10-21 have been added. Descriptive support for new claims 10 and 11 appears in the first full paragraph on page 30 and the third full paragraph on page 35, respectively; descriptive support for new claims 12-14 appears in the first full paragraph on page 34; and descriptive support for new claims 15 and 16 appears in the first full paragraph on page 30. New claim 17 finds descriptive support in original claim 3 (i.e., claim written in independent form), and new claims 18-21 find descriptive support in original claims 4 and 6-8, respectively. Claims 1, 2, and 6-21 are pending.

The objection to the specification is overcome by the above amendments. Although applicants disagree with the assertion made by the U.S. Patent and Trademark (“PTO”), the present claim language is clearly supported by the first full paragraph on page 30, along with the disclosure of the nucleic acid sequence of SEQ ID NO: 177 and the corresponding amino acid sequence of SEQ ID NO: 178.

The objections to claims 1 and 5 are overcome by the above amendments and should be withdrawn.

The rejection of claims 1-9 under 35 U.S.C. §112 (first paragraph) as lacking written descriptive support is respectfully traversed.

The burden of establishing that an application lacks adequate written descriptive support falls on the PTO. *See In re Wertheim*, 541 F.2d 257, 263, 191 USPQ 90, 97 (CCPA 1976) (“[T]he PTO has the initial burden of presenting evidence or reasons why persons skilled in the art would not recognize in the disclosure a description of the invention defined by the claims.”). Hence, the PTO must demonstrate *why* the disclosure is insufficient.

The Federal Circuit has clearly espoused that *per se* conclusions of written description violations cannot be founded upon the basis of genus size alone. *See Enzo Biochem, Inc. v. Gen-Probe Inc.*, 296 F.3d 1316, 1326-27, 63 USPQ2d 1609, 1614-15 (Fed. Cir. 2002) (refusing to adopt position that three species as a matter of law cannot satisfy written description requirement for significantly larger genus). Thus, the PTO’s conclusion

cannot be based on genus size alone. But that is precisely what the PTO has done at pages 3-4 of the outstanding office action. Because the PTO's position is unsupported by law and unsupported by any facts other than genus size, applicants submit that the PTO's position cannot be sustained.

In contrast, applicants present Exhibits 1-3 (attached hereto) as evidence that the nucleic acid sequence of SEQ ID NO: 177 and the corresponding amino acid sequence of SEQ ID NO: 178 represent the claimed genus. Exhibit 1 is a presentation of Genbank accessions for *Bacillus* or *Geobacillus* (formerly *Bacillus*) *hola* nucleic acids that are homologous to the nucleotide sequence of SEQ ID NO: 177. These *hola* nucleic acids were identified by a protein-protein BLAST search of the Genbank database performed using the amino acid sequence of SEQ ID NO: 178 and the BLAST default settings. Homologous sequences were identified in *Geobacillus kaustophilus*, *Bacillus cereus*, *Bacillus anthracis*, *Bacillus thuringiensis*, *Bacillus weihenstephanensis*, *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus halodurans*, and *Bacillus clausii* (Exhibit 1). Based upon alignments performed using Align[®] for nucleic acids and ClustalW for amino acids (using the European Molecular Biology Laboratory server and its default settings), these homologs share between about 51 and about 98 percent identity at the nucleic acid level (Exhibit 2) and between about 37 and about 99 percent identity at the amino acid level (Exhibit 3). Thus, species of delta subunits from organisms that belong to the biological classification *Bacillus* or *Geobacillus* clearly share similar structure and, therefore, function.

Applicants submit that the language recited in claims 1 and 9 is precisely the type of claim language that was acknowledged in *Univ. of California v. Eli Lilly*, 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) as being acceptable under the written description requirement. In *Eli Lilly*, the Federal Circuit addressed the validity of several claims of U.S. Patent No. 4,652,525 to Rutter et al. ("Rutter"), specifically those claims that recited the limitations 'vertebrate,' 'mammalian,' or 'human' cDNA for insulin. Rutter disclosed the nucleotide and amino acid sequences of a rat cDNA encoding insulin, but merely described a general procedure for obtaining the human cDNA encoding insulin. *Id.* at 1567, 43 USPQ2d at 1405. The Federal Circuit found that the description of the rat cDNA did not provide adequate descriptive support for the narrow subgenus of 'human' cDNA (no species disclosed), the larger subgenus of 'mammalian' cDNA (only the one rat species disclosed), and the larger genus of 'vertebrate' cDNA (only the one rat species disclosed). *Id.* at 1567-68, 43 USPQ2d at 1405. The Federal Circuit did acknowledge, however, the district court's

statement that the specification provided adequate written descriptive support for the subgenus of 'rat' cDNA encoding insulin. *Id.* at 1566.

Thus, functional language should be acceptable when the genus as claimed is sufficiently limited in scope (i.e., from *Bacillus* or *Bacillus stearothermophilus*) and the specification describes one or more species within that genus. Claims 1 and 9 recite the same type of functional claim language that was identified as acceptable in *Eli Lilly* given the description of a single species by its nucleotide sequence. Thus, it should be evident that claims 1 and 9 (and claims dependent thereon) find written descriptive support in the present application.

It should be noted that the "Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112 ¶ 1, 'Written Description' Requirement," make explicitly clear that the description of a representative number of species does *not* require the description to be of such a nature that it would provide support for each species that the genus embraces. 66 Fed. Reg. 1099, 1106 (2001). Hence, the absence of sequences (in the present specification) for the later-identified *holA* and delta homologs is irrelevant to the issue of whether the present specification provides adequate written descriptive support for their use in accordance with the present invention.

Moreover, the conclusion by the PTO is contrary to evidence submitted herewith by applicants. As demonstrated by Exhibits 1-3, one of ordinary skill in the art would have understood that applicants were in possession of the presently claimed invention at the time the present application was filed. This is so, because persons of skill in the art would have expected sufficiently related organisms from the genus *Bacillus* (and now *Geobacillus*) to possess homologous *holA* nucleotide sequences or delta subunit proteins. Exhibits 1-3 confirm this expectation to have been reasonable.

In view of all of the foregoing, applicants submit that the rejection of claims 1-9 is improper and should be withdrawn.

The rejection of claims 1-9 under 35 U.S.C. §112 (first paragraph) for lack of enablement is respectfully traversed.

It is the position of the PTO that the specification does not provide sufficient guidance for making and using other delta subunit-encoding DNA molecules within the scope of the claims. Applicants respectfully disagree.

The PTO is respectfully reminded that all that is needed is objective enablement of what is claimed. *In re Wright*, 999 F.2d 1557, 1561, 27 USPQ2d 1510, 1513 (Fed. Cir. 1993). The present application provides the nucleotide sequence of *Bacillus* (now

Geobacillus) *stearothermophilus hola* (e.g., SEQ ID NO: 177) and describes how one of ordinary skill can isolate homologs of the disclosed sequence (see page 41, line 9 to page 42, line 29), express the delta subunit encoded by such homologous *hola* sequences (see Example 19, expressing *A. aeolicus* delta subunit), and test the encoded delta subunit for clamp loader assembly competence (see Examples 24 and 25, testing *A. aeolicus* clamp loader assembly) and for clamp loader activity (see Examples 26 and 30, testing *A. aeolicus* clamp loader activity). Thus, one of ordinary skill in the art would have been fully able to make and use DNA molecules and their encoded proteins within the scope of the presently claimed invention.

Moreover, with regard to method 3 for homolog identification, described at page 42, that is precisely the approach used to identify the *hola* homologs shown in Exhibit 1 (i.e., from other *Bacillus* or *Geobacillus* organisms). For this reason, it should be apparent that the present application fully enables the production and use of other species of *Bacillus* or *Bacillus* (now *Geobacillus*) *stearothermophilus hola* homologs.

In view of all of the foregoing, applicants submit that the rejection of claims 1-9 for lack of enablement is improper and should be withdrawn.

Because 1 is allowable for the reasons noted above, applicants further submit that new claims 10-16 also are allowable. Consistent with the PTO acknowledgments at pages 3-4 the outstanding office action, applicants further submit that that the specification provides written descriptive support for and enables the claimed DNA molecules that encode the delta subunit including the amino acid sequence of SEQ ID NO: 178 (i.e., claims 17-21).

In view of all of the foregoing, applicant submits that this case is in condition for allowance and such allowance is earnestly solicited.

Respectfully submitted,

Date: August 24, 2006

/Edwin V. Merkel/

Edwin V. Merkel

Registration No. 40,087

NIXON PEABODY LLP
Clinton Square, P.O. Box 31051
Rochester, New York 14603-1051
Telephone: (585) 263-1128
Facsimile: (585) 263-1600

Exhibit 1

NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Display Show Send to

Range: from 2532557 to 2533603 ☐ Reverse complemented strand ☐ Fe

☐ 1: [BA000043](#). Reports *Geobacillus kaust...*[gi:56378377]

Links

Features Sequence

LOCUS BA000043 1047 bp DNA linear BCT 04-DEC-2004

DEFINITION *Geobacillus kaustophilus* HTA426 DNA, complete genome.

ACCESSION [BA000043](#) REGION: 2532557..2533603

VERSION BA000043.1 GI:56378377

KEYWORDS

SOURCE *Geobacillus kaustophilus* HTA426

ORGANISM *Geobacillus kaustophilus* HTA426
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Geobacillus*.

REFERENCE 1

AUTHORS Takami,H., Takaki,Y., Chee,G.J., Nishi,S., Shimamura,S., Suzuki,H., Matsui,S. and Uchiyama,I.

TITLE Thermoadaptation trait revealed by the genome sequence of thermophilic *Geobacillus kaustophilus*

JOURNAL (er) *Nucleic Acids Res.* 32 (21), 6292-6303 (2004)

PUBMED [15576355](#)

REFERENCE 2 (bases 1 to 1047)

AUTHORS Takami,H., Takaki,Y. and Chee,G.

TITLE Direct Submission

JOURNAL Submitted (25-JUN-2003) Hideto Takami, Japan Marine Science and Technology Center, Microbial Genome Analysis Research Group; 2-15 Natsushima-cho, Yokosuka, Kanagawa 237-0061, Japan
(E-mail:takamih@jamstec.go.jp,
URL:<http://www.jamstec.go.jp/jamstec-e/bio/exbase.html>,
Tel:81-46-867-9643, Fax:81-46-867-9645)

FEATURES

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ORIGIN

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Links

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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 REFERENCE 1 (bases 1 to 1041)
 AUTHORS Siefert, J., Ferreira, S., Johnson, J., Kravitz, S., Halpern, A.,
 Remington, K., Beeson, K., Tran, B., Rogers, Y.-H., Friedman, R. and
 Venter, J. C.
 TITLE Direct Submission
 JOURNAL Submitted (28-FEB-2006) J Craig Venter Institute, 9704 Medical
 Center Drive, Rockville, MD 20850, USA
 COMMENT Annotation was added by the NCBI Prokaryotic Genomes Automatic
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☐ 1: [NZ_AALL01000072](#). Reports *Bacillus cereus* s...[gi:89203481]

Links

Comment Features Sequence

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 DEFINITION *Bacillus cereus* subsp. cytotoxis NVH 391-98 ctg92, whole genome
 shotgun sequence.
 ACCESSION NZ_AALL01000072 REGION: complement(4223..5233)
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 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus*
cereus group.
 REFERENCE 1 (bases 1 to 1011)
 AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K.,
 Detter,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E.,
 Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S.,
 Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J.,
 Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S.,
 Nguen-the,C. and Sorokin,A.
 CONSRTM US DOE Joint Genome Institute (JGI-PGF)
 TITLE Sequencing of the draft genome and assembly of *Bacillus cereus*
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 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1011)
 AUTHORS Larimer,F. and Land,M.
 CONSRTM US DOE Joint Genome Institute (JGI-ORNL)
 TITLE Annotation of the draft genome assembly of *Bacillus cereus* subsp.
 NVH 391-98
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1011)
 AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K.,
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 Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S.,
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 Nguen-the,C. and Sorokin,A.
 CONSRTM US DOE Joint Genome Institute (JGI-PGF)
 TITLE Direct Submission
 JOURNAL Submitted (02-MAR-2006) US DOE Joint Genome Institute, 2800
 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
 COMMENT URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson (microbes@cuba.jgi-psf.org)
 Draft sequencing done at US DOE Joint Genome Institute
 Source DNA and bacteria available from Alexei Sorokin
 (alexei.sorokine@jouy.inra.fr)
 The JGI and collaborators endorse the principles for the
 distribution and use of large scale sequencing data adopted by the
 larger genome sequencing community and urge users of this data to
 follow them. It is our intention to publish the work of this

project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>)

Notes:

Bacillus cereus NVH 398-91 was originally isolated as a contaminant of vegetable puree in a retirement house in Essone (France) by Marie-Laure De Buyser (AFSSA, France). The strain was identified as a cause of a severe food poisoning case. It was further characterized biochemically and a novel cytotoxin K was identified as a major cause of epithelial cell lysis leading to necrotic enteritis (Lund et al, Mol Microbiol, 2000, 38, 254). Although the strain was identified as *Bacillus cereus*, it appeared to be different from all known strains. Detailed phylogenetic studies using MLST approach placed the strain rather far from main strain clusters, but confirmed that the strain belongs to the *B. cereus* group (Sorokin et al, Appl Env Microbiol, 2006, 72, 1569). Genomic sequence clearly indicated that the strain is very different from other representatives of the group and should be assigned a new species status, for which we propose a name *Bacillus cytotoxis*. However, assigning of the novel species status is hampered by the fact that only one such strain is described at the moment of genomic sequencing being done (2005).

FEATURES

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Show whole sequence

☐ Reverse complemented strand Fe☐ 1: [AE017334](#). Reports *Bacillus anthracis*...[gi:50082967]

Links

Comment Features Sequence

LOCUS AE017334 1011 bp DNA linear BCT 09-JUL-2004

DEFINITION *Bacillus anthracis* str. 'Ames Ancestor', complete genome.

ACCESSION [AE017334](#) REGION: 4137069..4138079

VERSION [AE017334.2](#) GI:50082967

KEYWORDS .

SOURCE *Bacillus anthracis* str. 'Ames Ancestor'

ORGANISM *Bacillus anthracis* str. 'Ames Ancestor'

Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1011)

AUTHORS Ravel,J., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z., Federova,N.B., Wilson,M., Stanley,S., Decker,S., Read,T.D., Salzberg,S. and Fraser,C.M.

TITLE *Bacillus anthracis* comparative genomics

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1011)

AUTHORS Ravel,J., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z., Federova,N.B., Salzberg,S. and Fraser,C.M.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

REFERENCE 3 (bases 1 to 1011)

AUTHORS Ravel,J., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z., Federova,N.B., Salzberg,S. and Fraser,C.M.

TITLE Direct Submission

JOURNAL Submitted (09-JUL-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

REMARK Sequence update by submitter

COMMENT On Jul 9, 2004 this sequence version replaced [gi:47500402](#).

FEATURES

source 1..1011

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CDS complement(1..1011)

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Display GenBank(Full) Show 5 Send to

Range: from 4085571 to 4086581

Show whole sequence

☐ Reverse complemented strand Fe☐ 1: NC_003909. Reports *Bacillus cereus* A...[gi:42779081]

Links

Comment Features Sequence

LOCUS NC_003909 1011 bp DNA linear BCT 17-JAN-2006

DEFINITION *Bacillus cereus* ATCC 10987, complete genome.

ACCESSION NC_003909 REGION: 4085571..4086581

VERSION NC_003909.8 GI:42779081

PROJECT GenomeProject:74

KEYWORDS .

SOURCE *Bacillus cereus* ATCC 10987

ORGANISM *Bacillus cereus* ATCC 10987
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1011)

AUTHORS Rasko,D.A., Ravel,J., Okstad,O.A., Helgason,E., Cer,R.Z., Jiang,L., Shores,K.A., Fouts,D.E., Tourasse,N.J., Angiuoli,S.V., Kolonay,J., Nelson,W.C., Kolsto,A.-B., Fraser,C.M. and Read,T.D.

TITLE The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic adaptations and a large plasmid related to *Bacillus anthracis* pX01

JOURNAL Nucleic Acids Res. 32 (3), 977-988 (2004)

PUBMED 14960714

REFERENCE 2 (bases 1 to 1011)

CONSRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (10-SEP-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 1011)

AUTHORS Rasko,D.A., Ravel,J., Okstad,O.A., Helgason,E., Cer,R.Z., Jiang,L., Shores,K.A., Fouts,D.E., Tourasse,N.J., Angiuoli,S.V., Kolonay,J., Nelson,W.C., Kolsto,A.-B., Fraser,C.M. and Read,T.D.

TITLE Direct Submission

JOURNAL Submitted (19-FEB-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from AE017194. On Feb 24, 2004 this sequence version replaced gi:29653128. COMPLETENESS: full length.

FEATURES

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Features: + Refresh

☐ 1: [NZ_AAJM01000393](#). Reports *Bacillus thuringi...*[gi:75763390]

Links

Features Sequence

LOCUS NZ_AAJM01000393 1011 bp DNA linear BCT 16-SEP-2005

DEFINITION *Bacillus thuringiensis* serovar israelensis ATCC 35646 sq1546, whole genome shotgun sequence.

ACCESSION NZ_AAJM01000393 REGION: complement(97..1107)

VERSION NZ_AAJM01000393.1 GI:75763390

KEYWORDS WGS.

SOURCE *Bacillus thuringiensis* serovar israelensis ATCC 35646

ORGANISM *Bacillus thuringiensis* serovar israelensis ATCC 35646
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 1011)

AUTHORS Anderson,I., Sorokin,A., Kapatral,V., Reznik,G., Bhattacharya,A., Mikhailova,N., Burd,H., Joukov,V., Kaznadzey,D., Walunas,T., D'Souza,M., Larsen,N., Pusch,G., Liolios,K., Grechkin,Y., Lapidus,A., Goltsman,E., Chu,L., Fonstein,M., Ehrlich,D., Overbeek,R., Kyrpides,N. and Ivanova,N.

TITLE Comparative genome analysis of *Bacillus cereus* group genomes with *Bacillus subtilis*

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1011)

AUTHORS Anderson,I., Sorokin,A., Kapatral,V., Reznik,G., Bhattacharya,A., Mikhailova,N., Burd,H., Joukov,V., Kaznadzey,D., Walunas,T., D'Souza,M., Larsen,N., Pusch,G., Liolios,K., Grechkin,Y., Lapidus,A., Goltsman,E., Chu,L., Fonstein,M., Ehrlich,D., Overbeek,R., Kyrpides,N. and Ivanova,N.

TITLE Comparative genome analysis of *Bacillus cereus* group genomes with *Bacillus subtilis*

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1011)

AUTHORS Anderson,I., Sorokin,A., Kapatral,V., Reznik,G., Bhattacharya,A., Mikhailova,N., Burd,H., Joukov,V., Kaznadzey,D., Walunas,T., D'Souza,M., Larsen,N., Pusch,G., Liolios,K., Grechkin,Y., Lapidus,A., Goltsman,E., Chu,L., Fonstein,M., Ehrlich,D., Overbeek,R., Kyrpides,N. and Ivanova,N.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-2005) Integrated Genomics, Inc., 2201 West Campbell Park Dr, Chicago, IL 60612, USA

REFERENCE 4 (bases 1 to 1011)

AUTHORS Anderson,I., Sorokin,A., Kapatral,V., Reznik,G., Bhattacharya,A., Mikhailova,N., Burd,H., Joukov,V., Kaznadzey,D., Walunas,T., D'Souza,M., Larsen,N., Pusch,G., Liolios,K., Grechkin,Y., Lapidus,A., Goltsman,E., Chu,L., Fonstein,M., Ehrlich,D., Overbeek,R., Kyrpides,N. and Ivanova,N.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-2005) Integrated Genomics, Inc., 2201 West Campbell Park Dr, Chicago, IL 60612, USA

FEATURES Location/Qualifiers

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ORIGIN

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☐ 1: [NZ_AAOY01000019](#). Reports *Bacillus weihenst...*[gi:89206281]

Links

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LOCUS NZ_AAOY01000019 1011 bp DNA linear BCT 06-MAR-2006
 DEFINITION *Bacillus weihenstephanensis* KBAB4 ctg244, whole genome shotgun sequence.
 ACCESSION [NZ_AAOY01000019](#) REGION: complement(8181..9191)
 VERSION [NZ_AAOY01000019.1](#) GI:89206281
 KEYWORDS WGS.
 SOURCE *Bacillus weihenstephanensis* KBAB4
 ORGANISM *Bacillus weihenstephanensis* KBAB4
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.
 REFERENCE 1 (bases 1 to 1011)
 AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K., Detter,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E., Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S., Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J., Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S., Nguen-the,C. and Sorokin,A.
 CONSRTM US DOE Joint Genome Institute (JGI-PGF)
 TITLE Sequencing of the draft genome and assembly of *Bacillus weihenstephanensis* KBAB4
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1011)
 AUTHORS Larimer,F. and Land,M.
 CONSRTM US DOE Joint Genome Institute (JGI-ORNL)
 TITLE Annotation of the draft genome assembly of *Bacillus weihenstephanensis* KBAB4
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1011)
 AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K., Detter,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E., Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S., Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J., Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S., Nuguen-the,C. and Sorokin,A.
 CONSRTM US DOE Joint Genome Institute (JGI-PGF)
 TITLE Direct Submission
 JOURNAL Submitted (02-MAR-2006) US DOE Joint Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
 COMMENT URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson (microbes@cuba.jgi-psf.org)
 Draft sequencing done at US DOE Joint Genome Institute
 Source DNA and bacteria available from Alexei Sorokin (alexei.sorokine@jouy.inra.fr)
 The JGI and collaborators endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to follow them. It is our intention to publish the work of this

project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>)

Notes:

Bacillus weihenstephanensis KBAB4 was originally isolated from forest soil near Versailles, France, and was originally identified as *Bacillus cereus* (Vilas-Boas et al, Appl Env Microbiol, 2002, 68, 1414). More detailed phylogenetic analysis, using MLST, of the Versailles Collection of *B. cereus* and *B. thuringiensis* strains revealed that the strain grows at low temperature (6°C) and clusters with many other strains able to grow at low temperatures, including the independently isolated and characterized strains WSBC10204 and WSBC10206 (Sorokin et al, Appl Env Microbiol, 2006, 72, 1569). The latter two strains are the type strains of a newly recognized species in the *B. cereus* group able to grow in cold and having the species name *Bacillus weihenstephanensis* (Lechner et al, Int. J. Syst. Bacteriol, 1998, 48, 1373). Since, by MLST, KBAB4 is very closely related to WSBC10204 and represents many other psychrotrophic strains, it was assigned a species name *Bacillus weihenstephanensis* and the strain KBAB4 should also be considered as a type representative of this species.

FEATURES

source	Location/Qualifiers
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ORIGIN

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Projection on the feature (#23)

Features: ☐ 1: [Z99117](#). Reports *Bacillus subtilis*...[gi:32468796][Links](#)[Comment](#) [Features](#) [Sequence](#)

LOCUS BSUB0014 1044 bp DNA linear BCT 18-APR-2005

DEFINITION *Bacillus subtilis* complete genome (section 14 of 21): from 2613658 to 2812830.

ACCESSION [Z99117](#) REGION: complement(21662..22705)

VERSION [Z99117.2](#) GI:32468796

KEYWORDS

SOURCE

ORGANISM *Bacillus subtilis* subsp. *subtilis* str. 168
Bacillus subtilis subsp. *subtilis* str. 168
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1 (bases 1 to 1044)

AUTHORS Kunst,F., Ogasawara,N., Moszer,I., Albertini,A.M., Alloni,G., Azevedo,V., Bertero,M.G., Bessieres,P., Bolotin,A., Borchert,S., Borriess,R., Boursier,L., Brans,A., Braun,M., Brignell,S.C., Bron,S., Brouillet,S., Bruschi,C.V., Caldwell,B., Capuano,V., Carter,N.M., Choi,S.K., Codani,J.J., Connerton,I.F., Cummings,N.J., Daniel,R.A., Denizot,F., Devine,K.M., Dusterhoft,A., Ehrlich,S.D., Emmerson,P.T., Entian,K.D., Errington,J., Fabret,C., Ferrari,E., Foulger,D., Fritz,C., Fujita,M., Fujita,Y., Fuma,S., Galizzi,A., Galleron,N., Ghim,S.Y., Glaser,P., Goffeau,A., Golightly,E.J., Grandi,G., Guiseppi,G., Guy,B.J., Haga,K., Haiech,J., Harwood,C.R., Henaut,A., Hilbert,H., Holsappel,S., Hosono,S., Hullo,M.F., Itaya,M., Jones,L., Joris,B., Karamata,D., Kasahara,Y., Klaerr-Blanchard,M., Klein,C., Kobayashi,Y., Koetter,P., Koningstein,G., Krogh,S., Kumano,M., Kurita,K., Lapidus,A., Lardinois,S., Lauber,J., Lazarevic,V., Lee,S.M., Levine,A., Liu,H., Masuda,S., Mauel,C., Medigue,C., Medina,N., Mellado,R.P., Mizuno,M., Moestl,D., Nakai,S., Noback,M., Noone,D., O'Reilly,M., Ogawa,K., Ogiwara,A., Oudega,B., Park,S.H., Parro,V., Pohl,T.M., Portetelle,D., Porwollik,S., Prescott,A.M., Presecan,E., Pujic,P., Purnelle,B., Rapoport,G., Rey,M., Reynolds,S., Rieger,M., Rivolta,C., Rocha,E., Roche,B., Rose,M., Sadaie,Y., Sato,T., Scanlan,E., Schleich,S., Schroeter,R., Scoffone,F., Sekiguchi,J., Sekowska,A., Seror,S.J., Serror,P., Shin,B.S., Soldo,B., Sorokin,A., Tacconi,E., Takagi,T., Takahashi,H., Takemaru,K., Takeuchi,M., Tamakoshi,A., Tanaka,T., Terpstra,P., Tognoni,A., Tosato,V., Uchiyama,S., Vandenbol,M., Vannier,F., Vassarotti,A., Viari,A., Wambutt,R., Wedler,E., Wedler,H., Weitzenegger,T., Winters,P., Wipat,A., Yamamoto,H., Yamane,K., Yasumoto,K., Yata,K., Yoshida,K., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and Danchin,A.

TITLE The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*

JOURNAL *Nature* 390 (6657), 249-256 (1997)

PUBMED [9384377](#)

REFERENCE 2 (bases 1 to 1044)

AUTHORS Kunst,F., Ogasawara,N., Yoshikawa,H. and Danchin,A.

TITLE Direct Submission

JOURNAL Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur, Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48

COMMENT On Jul 7, 2003 this sequence version replaced gi:2634966. This entry contains data from release R16.1 of the Subtilist database. Further data on gene annotation and detailed information about changes from previous releases can be found at <http://genolist.pasteur.fr/Subtilist/>.

FEATURES

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	/note="similar to unknown proteins"
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	/db_xref="Subtilist:BG11642"
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ORIGIN

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Range: from 2643434 to 2644498

Show whole sequence

☐ Reverse complemented strand Fe☐ 1: CP000002. Reports *Bacillus lichenif...*[gi:56160984]

Links

Comment Features Sequence

LOCUS CP000002 1065 bp DNA linear BCT 03-DEC-2004

DEFINITION *Bacillus licheniformis* ATCC 14580, complete genome.

ACCESSION CP000002 REGION: 2643434..2644498

VERSION CP000002.2 GI:56160984

KEYWORDS .

SOURCE *Bacillus licheniformis* ATCC 14580 (DSM 13)

ORGANISM *Bacillus licheniformis* ATCC 14580
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1 (bases 1 to 1065)

AUTHORS Rey,M.W., Ramaiya,P., Nelson,B.A., Brody-Karpin,S.D.,
Zaretsky,E.J., Tang,M., de Leon,A.L., Xiang,H., Gusti,V.,
Clausen,I.G., Olsen,P.B., Rasmussen,M.D., Andersen,J.T.,
Jorgensen,P.L., Larsen,T.S., Sorokin,A., Bolotin,A., Lapidus,A.,
Galleron,N., Ehrlich,S.D. and Berka,R.M.

TITLE Complete genome sequence of the industrial bacterium *Bacillus licheniformis* and comparisons with closely related *Bacillus* species

JOURNAL Genome Biol. 5 (10), R77 (2004)

PUBMED 15461803

REFERENCE 2 (bases 1 to 1065)

AUTHORS Berka,R.M., Rey,M.W. and Ramaiya,P.

TITLE Direct Submission

JOURNAL Submitted (14-JUL-2004) Novozymes Biotech Inc, 1445 Drew Ave,
Davis, CA 95616, USA

REFERENCE 3 (bases 1 to 1065)

AUTHORS Berka,R.M., Rey,M.W. and Ramaiya,P.

TITLE Direct Submission

JOURNAL Submitted (29-SEP-2004) Novozymes Biotech Inc, 1445 Drew Ave,
Davis, CA 95616, USA

REMARK Sequence update by submitter

COMMENT On Dec 1, 2004 this sequence version replaced gi:52001702.

FEATURES

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/db_xref="taxon:279010"
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ORIGIN

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Range: from 1421231 to 1422259

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☐ Reverse complemented strand Fe☐ 1: BA000004. Reports *Bacillus halodura*...[gi:47118318]

Links

Comment Features Sequence

LOCUS BA000004 1029 bp DNA linear BCT 01-DEC-2004

DEFINITION *Bacillus halodurans* C-125 DNA, complete genome.

ACCESSION BA000004 REGION: 1421231..1422259

VERSION BA000004.3 GI:47118318

KEYWORDS .

SOURCE *Bacillus halodurans* C-125

ORGANISM *Bacillus halodurans* C-125
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1

AUTHORS Takami,H.

TITLE Genome analysis of facultatively alkaliphilic *Bacillus halodurans* C-125

JOURNAL (in) Horikoshi,K. and Tsujii,K. (Eds.);
EXTREMOPHILES IN DEEP-SEA ENVIRONMENTS: 249-284;
Springer-Verlag (1999)

REFERENCE 2

AUTHORS Takami,H. and Horikoshi,K.

TITLE Reidentification of facultatively alkaliphilic *Bacillus* sp. C-125 to *Bacillus halodurans*

JOURNAL Biosci. Biotechnol. Biochem. 63, 943-945 (1999)

REFERENCE 3

AUTHORS Takami,H., Nakasone,K., Hiramata,C., Takaki,Y., Masui,N., Fuji,F., Nakamura,Y. and Inoue,A.

TITLE An improved physical and genetic map of the genome of alkaliphilic *Bacillus* sp. C-125

JOURNAL Extremophiles 3 (1), 21-28 (1999)

PUBMED 10086841

REFERENCE 4

AUTHORS Takami,H., Nakasone,K., Ogasawara,N., Hiramata,C., Nakamura,Y., Masui,N., Fuji,F., Takaki,Y., Inoue,A. and Horikoshi,K.

TITLE Sequencing of three lambda clones from the genome of alkaliphilic *Bacillus* sp. strain C-125

JOURNAL Extremophiles 3 (1), 29-34 (1999)

PUBMED 10086842

REFERENCE 5

AUTHORS Takami,H., Takaki,Y., Nakasone,K., Hiramata,C., Inoue,A. and Horikoshi,K.

TITLE Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic *Bacillus* sp. strain C-125

JOURNAL Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)

PUBMED 10192928

REFERENCE 6

AUTHORS Takami,H., Masui,N., Nakasone,K. and Horikoshi,K.

TITLE Replication origin region of the chromosome of alkaliphilic *Bacillus halodurans* C-125

JOURNAL Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)

PUBMED 10427704

REFERENCE 7
AUTHORS Takami,H., Takaki,Y., Nakasone,K., Sakiyama,T., Maeno,G.,
Sasaki,R., Hirama,C., Fuji,F. and Masui,N.
TITLE Genetic analysis of the chromosome of alkaliphilic *Bacillus*
halodurans C-125
JOURNAL *Extremophiles* 3 (3), 227-233 (1999)
PUBMED [10484179](#)

REFERENCE 8
AUTHORS Takami,H. and Horikoshi,K.
TITLE Analysis of the genome of an alkaliphilic *Bacillus* strain from an
industrial point of view
JOURNAL *Extremophiles* 4 (2), 99-108 (2000)
PUBMED [10805564](#)

REFERENCE 9
AUTHORS Nakasone,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T.,
Hirama,C., Fuji,F. and Takami,H.
TITLE Characterization and comparative study of the *rrn* operons of
alkaliphilic *Bacillus halodurans* C-125
JOURNAL *Extremophiles* 4 (4), 209-214 (2000)
PUBMED [10972189](#)

REFERENCE 10
AUTHORS Takami,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N.,
Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and
Horikoshi,K.
TITLE Complete genome sequence of the alkaliphilic bacterium *Bacillus*
halodurans and genomic sequence comparison with *Bacillus subtilis*
JOURNAL *Nucleic Acids Res.* 28 (21), 4317-4331 (2000)
PUBMED [11058132](#)

REFERENCE 11 (bases 1 to 1029)
AUTHORS Takami,H. and Takaki,Y.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and
Technology Center, Deep-sea Microorganisms Research Group; 2-15
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
(E-mail:takamih@jamstec.go.jp,
URL:<http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html>,
Tel:81-468-67-3895, Fax:81-468-66-6364)

COMMENT On or before Dec 8, 2004 this sequence version replaced
[gi:10172612](#), [gi:10172890](#), [gi:10173176](#), [gi:10173440](#), [gi:10173727](#),
[gi:10174030](#), [gi:10174345](#), [gi:10174613](#), [gi:12641879](#), [gi:10175192](#),
[gi:10175500](#), [gi:10175792](#), [gi:10176109](#), [gi:10176401](#).

FEATURES Location/Qualifiers
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ORIGIN

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1021  gtaggttag
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☐ Reverse complemented strand Fe☐ 1: AP006627. Reports *Bacillus clausii* ...[gi:56908016]

Links

Features Sequence

LOCUS AP006627 1023 bp DNA linear BCT 28-JUL-2006

DEFINITION *Bacillus clausii* KSM-K16 DNA, complete genome.

ACCESSION AP006627 REGION: 1778796..1779818

VERSION AP006627.1 GI:56908016

KEYWORDS

SOURCE

ORGANISM *Bacillus clausii* KSM-K16
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1

AUTHORS Hakamada,Y., Kobayashi,T., Hitomi,J., Kawai,S. and Ito,S.

TITLE Molecular cloning and nucleotide sequence of the gene for an alkaline protease from the alkalophilic *Bacillus* sp. KSM-K16

JOURNAL J. Ferment. Bioeng. 78, 105-108 (1994)

REFERENCE 2

AUTHORS Kobayashi,T., Hakamada,Y., Adachi,S., Hitomi,J., Yoshimatsu,T., Koike,K., Kawai,S. and Ito,S.

TITLE Purification and properties of an alkaline protease from alkalophilic *Bacillus* sp. KSM-K16

JOURNAL Appl. Microbiol. Biotechnol. 43 (3), 473-481 (1995)

PUBMED 7632397

REFERENCE 3

AUTHORS Shirai,T., Suzuki,A., Yamane,T., Ashida,T., Kobayashi,T., Hitomi,J. and Ito,S.

TITLE High-resolution crystal structure of M-protease: phylogeny aided analysis of the high-alkaline adaptation mechanism

JOURNAL Protein Eng. 10 (6), 627-634 (1997)

PUBMED 9278275

REFERENCE 4

AUTHORS Sakaki,Y., Kageyama,Y., Shimamura,S., Suzuki,H., Nishi,S., Hatada,Y., Kawai,S., Ito,S. and Horikoshi,K.

TITLE The complete genome sequence of the alkaliphilic *Bacillus clausii* KSM-K16

JOURNAL Unpublished

REFERENCE 5 (bases 1 to 1023)

AUTHORS Sakaki,Y., Kageyama,Y., Shimamura,S., Suzuki,H., Nishi,S., Hatada,Y., Kawai,S., Ito,S. and Horikoshi,K.

TITLE Direct Submission

JOURNAL Submitted (19-OCT-2003) Yasushi Kageyama, Kao Corporation, Biological Science Laboratories; 2606 Akabane, Ichikai-machi, Haga-gun, Tochigi 321-3497, Japan
(E-mail:kageyama.yasushi@kao.co.jp, URL:http://www.kao.co.jp/e/, Tel:81-285-68-7516, Fax:81-285-68-7547)

FEATURES

source Location/Qualifiers

1..1023

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1021 taa
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//

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Aug 15 2006 13:27:38

Exhibit 2

#####

Program: needle
Rundate: Wed Aug 23 05:38:23 2006
Align_format: srspair
Report_file: /ebi/extserv/old-work/needle-20060823-05382260401273.output
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2: G_kaustophilu
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Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 1047
Identity: 1030/1047 (98.4%)
Similarity: 1030/1047 (98.4%)
Gaps: 3/1047 (0.3%)
Score: 6325.0

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SEQ_177	51	TTATTTATTATACGGCAATGAGCCGTTTTTTATTAACGGAAACGTATGAGC	100
G_kaustophilu	51	ttatattattatacggcaatgagccgtttttattaacggaaacgtatgagc	100
SEQ_177	101	GATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACTTGGCT	150
G_kaustophilu	101	gattggtgaacgcagcgcttggccccgaggagcgaggagtggaacttggt	150
SEQ_177	151	GTGTACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGGCCGA	200
G_kaustophilu	151	gtgtacgactgcgaggaaacgccggtcgaggcgcgcttgaggaggccga	200
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G_kaustophilu	201	gacggtgccgtttttcggcgagcgcggtgtcatcctcatcaagcatccat	250
SEQ_177	251	ATTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTGGCGAAG	300
G_kaustophilu	251	attttttcacgtctgaaaaagagaaggagatcgaacatgatttggcgaag	300
SEQ_177	301	CTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCTTTT	350
G_kaustophilu	301	ctggaggcgctacttgaaggcgccgctcgccgttttcgatcgtcgtctttt	350
SEQ_177	351	CGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCTCGCCA	400
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SEQ_177	401	AAGAGCAAAGCGAAGTCGTTCATCGCCGCCCGCTCGCCGAAGCGGAGCTG	450
G_kaustophilu	401	aagagcaaagcgaagtcgtcatcgccgcccgctcgccgaagcggagctg	450
SEQ_177	451	CGTGCCTGGGTGCGGCGCCGCATCGAGAGCCAAGGGGCGCAAGCAAGCGA	500
G_kaustophilu	451	cgcgcctgggtgcgcgccgcgcatcgagagccaagggcgcaagcaagcga	500

SEQ_177	501	CGAGGCGATTGATGTCTGTGTCGGCGGGCCGGGACGCAGCTTTCGCCT	550
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SEQ_177	551	TGGCGAATGAAATCGATAAATTGGCCCTGTTTGCCGGATCGGGCGGAACC	600
G_kaustophilu	551	tggcgaatgaaatcgataaattggccctgtttgccggatcgggcggaacc	600
SEQ_177	601	ATCGAGGCGGCGGCGGTTGAGCGGCTTGTCGCCCGCACGCCGAAGAAAA	650
G_kaustophilu	601	atcgaggcgggcggttgaaacggttgctgcgccgcacgccggaagaaaa	650
SEQ_177	651	CGTATTGTGCTTGTTCGAGCAAGTGGCGAAGCGCGACATTCCAGCAGCGT	700
G_kaustophilu	651	cgtatttgtgcttgtcgcagcaagtggcgaagcgcgacattccagcggcgt	700
SEQ_177	701	TGCAGACGTTTTATGATCTGCTTGAAAACAATGAAGAGCCGATCAAAATT	750
G_kaustophilu	701	tgcaaacgttttatgatctgcttgaaaacaatgaagagccgatcaaaatt	750
SEQ_177	751	TTGGCGTTGCTCGCCGCCCATTTCCGCTTGCTTTCGCAAGTGAAATGGCT	800
G_kaustophilu	751	ttggcgctgctcgccgccatttccgcttgctttcgcaagtgaaatggct	800
SEQ_177	801	TGCCTCCTTAGGCTACGGACAGGCGCAAATTGCTGCGGCGCTCAAGGTGC	850
G_kaustophilu	801	tgcttccttaggctacgggcaggcgcaaattgctgcggcgctcaaggtgc	850
SEQ_177	851	ACCCGTTCCGCGTCAAGCTCGCTCTTGCTCAAGCGGCCCGCTTCGCTGAC	900
G_kaustophilu	851	acccgttcgcgctcaagctcgctcttgctcaagcgcccgcttcgctgac	900
SEQ_177	901	GGAGAGCTTGCTGAGGCGATCAACGAGCTCGCTGACGCCGATTACGAAGT	950
G_kaustophilu	901	ggagagcttgctgaggcgatcaacgagctcgctgacgccgattacgaagt	950
SEQ_177	951	GAAAAGCGGGGCGGTCGATCGCCGGTTGGCCGTTGAGCTGCTTCTGATGC	1000
G_kaustophilu	951	gaaaagcgggagcggtcgatcgccggttgccggttgagctgcttctgatgc	1000
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# Extend_penalty: 0.5
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# Length: 1090
# Identity: 648/1090 (59.4%)
# Similarity: 648/1090 (59.4%)
# Gaps: 95/1090 ( 8.7%)
# Score: 3106.0
#
#
#=====

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Bacillus_sp_N 97 cagctgcttatcaacaatgtgctgg---ctgaaga-cgagagcgatttta 142

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Bacillus_sp_N 143 atctgtctacatatgatttggaggaaacaccaatagaagcggcacttgag 192

SEQ_177 193 GAGGCCGAGACGGTGCCGTTTTTTCGGCG--AGCGCGTGTCATTCTCAT 239
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Bacillus_sp_N 193 gatgcagagaccttccctttcatgggggataagaggctcatctttcttca 242

SEQ_177 240 CAAGCATCCATATTTTTTTTACGTCTGAAAA--AGAGAAGGAGATCGAAC 286
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Bacillus_sp_N 243 caa-c--ccctcttttctgacttccgaaaagacaaagggaagactgagc 289

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SEQ_177 337 ATCGTCGTCTTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAAT 386
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Bacillus_sp_N 390 tacgaag-gaactgaagaaaaaagc-aagt-gtccttgaggccaaaaaac 436

SEQ_177 434 TCGCCGAAGC-GGAGCTGCGTGCCTGGGTGCGGCGCCGCATCGAGAGCCA 482
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Bacillus sp N 437 t-gggggagcaggagctgaaagtctggatcagg---gaaagggtgccc 481
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SEQ_177	526	--CGGGCCGGGAC--GCAGCTTTCGCCCTTGGCGAATGAAATCGATAAAT	571
Bacillus_sp_N	527	ctctggcaggtaccaacctctttatgc--tgacaggtgaaattgataaat	574
SEQ_177	572	TGGCCCTGTTTGCCGGATCGGGCGGAACC--ATCGAGGCGGCGCGGTTG	619
Bacillus_sp_N	575	tggccttatatgccg--acgaggaaaagctgattgatgccgaggcagttg	622
SEQ_177	620	AGCGGCTTGTCGCCCCGACGCCGAAGAAAACGTATTGTGCTTGTGCGAG	669
Bacillus_sp_N	623	acaagctggttgccaggtcgcttgagcagaatattttcacccctgtcgac	672
SEQ_177	670	CAAGTGGCGAAGCGCGACATTCCAGCAGCGTTGCAGACGTTTTATGATCT	719
Bacillus_sp_N	673	aagtggtccacagaaaaatagatgaggcactgcggattttattatgatct	722
SEQ_177	720	GCTTGAAAACAATGAAGAGCCGATCAAAATTTTGGCGTTGCTCGCCGCC	769
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SEQ_177	770	ATTTCCGCTTGCTTTTCGCAAGTGAATGGCTTGCCCTCCTTAGGCTACGGA	819
Bacillus_sp_N	773	aattcaggctgatctaccaggtgaaggagctttcgagaaggggatacggc	822
SEQ_177	820	CAGGCGCAAATTGCTGCGGC--GC-TCAAGGTGCACCCGTTCCGCGTCAAG	867
Bacillus_sp_N	823	cagcagcagacggc--cgataacttaaaggtccatcccttcagggtcaag	870
SEQ_177	868	CTCGCTCTTGCTCAAGCGGCCCGC--TTCGCTGACGGAGAGCTTGCTGAG	915
Bacillus_sp_N	871	cttcagccggacaggc--ccagcttttcggagatgaagaactgtcc---	915
SEQ_177	916	GCG-ATCAACGAGC-TC--GCTGACGCCGATTACGAAGTGAAAAGCGGGG	961
Bacillus_sp_N	916	-cgcacatgaagcttctggcagaagcagattatgagatgaaaa-caggg	963
SEQ_177	962	CGGTCGATCGCCGGTTGGC-CGTTGAGCTGCTTCTGATGCGCTGGGGCGC	1010
Bacillus_sp_N	964	gggatgaacaaggaaatgcttattgagatgtttttgtt---cag---gc	1006
SEQ_177	1011	CCGCCCCGGCGCAAGCGGGCGCCAC--GGCCGGCGG	1044
Bacillus_sp_N	1007	tc-cacgac-catgc---cctccacaaacagacaaaataa	1041

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Extend_penalty: 0.5

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Identity: 582/1072 (54.3%)
Similarity: 582/1072 (54.3%)
Gaps: 89/1072 (8.3%)
Score: 2732.0

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SEQ_177	50	TTTATTATTATACGGCAATG-AGCCGTTTTTATTAACGGAAACGTATGA	98
		
B_cereus_subs	47	tttatttattgtatggaacggaagcctattttataaat-gaaac----aa	91
SEQ_177	99	GCGATTGGTGAAC----GCAGCGCTTGGCCCCGAGGAGCGGGAGTGAAC	144
		
B_cereus_subs	92	tcgatttaattacagtagaggcacttgccgaagaagatcgtgattttaat	141
SEQ_177	145	TTGGCTGTGTACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGA	194
		
B_cereus_subs	142	attgttacatatgatttagaagaggcgtatttagaggatgtagtagagga	191
SEQ_177	195	GGCCGAGACGGTGCCGTTTTTCGGCGAGCGGCGTGTCTCTCATCAAGC	244
		
B_cereus_subs	192	tgcaaggacgcttccattcttggagagcgaaaaatattattaataaagt	241
SEQ_177	245	ATCCATATTTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTG	294
		
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SEQ_177	295	GCGAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGT	344
		
B_cereus_subs	289	aaaatccttgaggaatatattgctgaaccatctccattttcgcgcatgat	338
SEQ_177	345	CTTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGC	394
		
B_cereus_subs	339	ttttatcgctccatagaaaagttagatgagcgaaaaaaaattacgaag-	387
SEQ_177	395	TCGCCAAAGAGCAAAGC-GAAGTCGTCATCGC---CGCCCCGCTCGCCGA	440
		
B_cereus_subs	388	ttattaaagaaaaacggtgaggttagagaagcgaatgctatgcaagtaca	437
SEQ_177	441	AGCGGAGCTGCGTGCCTGGGTGCGGCGCCGCATCGAGAGCC-AAGGGGCG	489
		
B_cereus_subs	438	agatg---ttaggaatggat-----tgtaaagcgtgctgaagaagtt	477

SEQ_177	490	CA--AGCAAG-CGACGAGGCGATTG--ATGTCCTGTTGCGGCGGGCCGG	533
B_cereus_subs	478	catgtgcatgttgaagaggcggtgtaagtttgcttttgagctcgtagg	527
SEQ_177	534	GACGCAGCTTTCGCC- TTGGCGAATGAAATCGATAAATTGGCCCTGTTT	582
B_cereus_subs	528	ga-gcaatgtaacaatgtagcaaaggaaatggataagttaacactgtat	576
SEQ_177	583	GCCGGATCGGGCGGAACCATCGAGCGGCGCGGTGAGCG--GCTTGT	629
B_cereus_subs	577	gttggaaacggcgagacatt--acaacaaaacttgtaagtgaacttgt	623
SEQ_177	630	CGCCCGCACGCCG--GAAGAAAACGTATTTGTGCTTGTC-GAGCAAGTGG	676
B_cereus_subs	624	--accgaagtcagttgagcaaatgttttgc-cttaacagaaaaagtcg	670
SEQ_177	677	CGAAGCGCGACATTCCAGCAGCGTTGCAGACGTTTATGATCTGCTTGAA	726
B_cereus_subs	671	taaaaaagatatagcaggagcaatgaaaatattagatggcttatttaca	720
SEQ_177	727	AACAATGAAGAGCCGATCAAAATTTTGGCGTTGCTCGCCGCCATTTCGG	776
B_cereus_subs	721	caacaggaagaaccaattaaattattagcgttgctagtgagtcaattccg	770
SEQ_177	777	CTTGCTTTCGCAAGTGAAATGGCT--TGCCTCCTTAGGCTACGGACAGGC	824
B_cereus_subs	771	tttattacatcaagtaaaagaactacagcagc--gaggatacggacaaaa	818
SEQ_177	825	GCAAATTGCTGCGGCGCTCAAGGTG--CACCCGTTCCGCGTCAAGCTCGC	872
B_cereus_subs	819	tcaaattgcttc-gc-atattggtgttcacgtaccgagtaaaattggc	866
SEQ_177	873	TCTTGCTCAAGCGGCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATCA	922
B_cereus_subs	867	gatgaatcaaacgaaacttttctcatttgaagaattgaaaaaggtaattt	916
SEQ_177	923	ACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGGCGGTTCGATCGC	972
B_cereus_subs	917	tcgagttagcgggaagcgactatagtatgaaaacagggaaaatggataag	966
SEQ_177	973	CGGTTGGCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCGCGCA	1022
B_cereus_subs	967	aagttagttctagaattttcttaatg-----agactgaatca	1004
SEQ_177	1023	AGCGGGGCGCCACGGCCGCGG	1044
B_cereus_subs	1005	tatgtga	1011

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# Rundate:  Wed Aug 23 14:53:14 2006
# Align_format:  srspair
# Report_file:  /ebi/extserv/old-work/needle-20060823-14531389444774.output
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# 1: SEQ_177
# 2: B_anthraxis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
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# Length: 1066
# Identity:      585/1066 (54.9%)
# Similarity:    585/1066 (54.9%)
# Gaps:          77/1066 ( 7.2%)
# Score: 2717.0
#
#
#=====

SEQ_177      1  ATGC-TGGAACGCGTATGGGGAACATTGAAAAACGGCGTTTTTCTCCCC      49
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B_anthraxis  1  atgagtgatatacata----aaaagattaaaaaaaagcagtttgctccgt      46

SEQ_177      50  TTTATTATTATTATACGGCAATGAGCCGTTTTTTATTAAACGGAAACGTATGAG      99
      |. |||||..|. ||..|..|..| |..||.. |||||..||.. |||||..|..|
B_anthraxis  47  tgtatttactgtatggaacggaagcggtttttataaatgaaacgataaag      96

SEQ_177     100  CGATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACTTGGC      149
      |...|...|..|..| ||||| |||...| |..| |..| |||||..| |. |.
B_anthraxis  97  cttattacaacagaagcgcttgaagaggaagatcgcgagttaat---gt      143

SEQ_177     150  TGTG---TACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGG      196
      |||| | |..|..|..| |..| |..|..| |..| |..| |..| |..| |
B_anthraxis 144  tgtgacatatgatttagaagaagcgtatttagaagatgtggttgaggatg      193

SEQ_177     197  CCGAGACGGTGCCGTTTTTTCGGCGAGCGGCGTGTTCATTCTCATCAAGCAT      246
      |...| |..| |..| ||||| |||..| |..| |..| |..| |..| |..|
B_anthraxis 194  cacgtacacttccttttttcggagaacgtaaagtgttattaataaaatca      243

SEQ_177     247  CCATATTTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTGGC      296
      ||||..| |||||..| |||||..| | |..| |..| |..| |..| |..|
B_anthraxis 244  ccattatttttaacgtcacaaaaagaaa---agttagaacaaaatataaa      290

SEQ_177     297  GAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCT      346
      .|...| |..| |..| |..| |..| |..| |..| |..| |..| |..| |..|
B_anthraxis 291  aattttagaagaatatatcggggaaccttctccattttctattcttgttt      340

SEQ_177     347  TTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCTC      396
      ||..| |||||..| |||||..| |||||..| |||||..| |||||..| ||..|
B_anthraxis 341  ttgttgcgcccttacgaaaagccttgatgaacgaaaaaaaattacaaaact-      389

SEQ_177     397  GCCAAAGAGCAAAGC-GAAGTCGTATCGCCGCCCGCTCGCCGAAGCGG      445
      ...| |||||..| | | |..| |..| |..| |..| |..| |..| |..|
B_anthraxis 390  attaaagaaaacagcagatatagtagaagcgaatgcgat-gcaagtgcag      438

SEQ_177     446  AGCTGCGTGCCTGGGTGCGGCGCCGCATCGAG-AGCCAAGGGGC---GC      490
      |. | |..| |..| |..| |..| |..| |..| |..| |..| |..| |..|
B_anthraxis 439  -gat--gttcaaaagtggattgtagc-tcgtgcagaggaagggcatgtac      484
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SEQ_177	491	AAGCAAGCGACGAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGACGCAG	540
B_anthraxis	485	atattgataaatgcagctgttagtttattgttagagcttg-tgggaagtaa	533
SEQ_177	541	CTTTCGCC- TTGGCGAATGAAATCGATAAATTGCCCTGTGTTGCCGGAT	589
B_anthraxis	534	tgtgacgatgttggcgaaggaaatggacaagttaacgttatacgtcggtta	583
SEQ_177	590	CGGGCGGAACCATCGAGGCGGCGCGGTTGAGCGGCTTGTCGCCCCGCACG	639
B_anthraxis	584	tgggcggagagattacgccgaaacttggtgcagagcttgt-gccaaat-	631
SEQ_177	640	CCG--GAAGAAAACGTATTGTTGCTTGTCGAGCAAGTGGCGAAGCGCGAC	687
B_anthraxis	632	cagttgaacaaaatgtatttgctttaacagaaaaagtggtaaaaaaagat	681
SEQ_177	688	ATCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAAAACAATGAAGA	737
B_anthraxis	682	atcgcaggtgcatgcaaattttggtatggattatttacgcagcaggagga	731
SEQ_177	738	GCCGATCAAAATTTGGCGTTGCTCGCCGCCCATTTCCGCTTGCTTTCGC	787
B_anthraxis	732	accgattaaattgcttgcgttggttagtaagtcaattccgcttgctgcac	781
SEQ_177	788	AAGTGAAATGGCTTGCCCTC--CTTAGGCTACGGACAGGCGCAAATTGCTG	835
B_anthraxis	782	aagtaaaagag-ttacagcagcgt-ggttatggacaaaatcaaattgct-	828
SEQ_177	836	CGGCGCTCA--AGGTG--CACCCGTTCCGCGTCAAGCTCGCTCTTGCTC	880
B_anthraxis	829	----tctcatattggtgtacatccatatcgtgtaaagtttagcatgaatc	874
SEQ_177	881	AAGCGGCCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATCAACGAGCTC	930
B_anthraxis	875	aaacgaagtttttctcttttgaagaactaaaaaaagtgattatagaattg	924
SEQ_177	931	GCTGACGCCGATTACGAAGTGAAAAGCGGGCGGTCGAT-CGCCGGTTG-	978
B_anthraxis	925	gcggaagctgattatagtatgaagactggaaaaatggataagaaacttgt	974
SEQ_177	979	GCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCCGCCGCGCAAGCGGG	1028
B_anthraxis	975	gc--ttgagtttttcttaatgcat-----taaatcatatgtga	1011
SEQ_177	1029	GCGCCACGGCCGGCGG	1044
B_anthraxis	1012		1011


```
#####
# Program: needle
# Rundate: Wed Aug 23 15:01:17 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060823-15011448417323.output
#####

#=====
#
# Aligned_sequences: 2
# 1: SEQ_177
# 2: B_cereus
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1076
# Identity: 588/1076 (54.6%)
# Similarity: 588/1076 (54.6%)
# Gaps: 97/1076 ( 9.0%)
# Score: 2650.0
#
#
#=====

SEQ_177      1 ATGC-TGGAACGCGTATGGGAAAACATTGAAAAACGGCGTTTTTCTCCCC      49
      |||. ||..||..|||   .|||.|||.|||||...||..|||.||||..
B_cereus     1 atgagtgatatacata----aaaagattaaaaagaagcagtttgctccgt      46

SEQ_177      50 TTTATTATTATACGGCAATGAGCCGTTTTTTATTAAACGGAAACGTATGAG      99
      |.|||||.|||||.||..||..|||||||.|||.|||||||....||
B_cereus     47 tatatttactatatggaacagaagcgttttttataaatgaaacgataaag      96

SEQ_177     100 CGATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACCTGGC      149
      |...|...|...|..|||||||.....|..|||.|||.||||..|.
B_cereus     97 cttattacaacagaagcgcttgaagaggaagatcgcgagtttaat---gt      143

SEQ_177     150 TGTG---TACGACTGCGAGGAAACGCCGATCGAGCGGCGCTTGAGGAGG      196
      ||||   |||.||..|||.|||||......|..|||.||..|||.|||
B_cereus    144 tgtgacatatgatttagaagaagcatatttagaagatgtggttgaggatg      193

SEQ_177     197 CCGAGACGGTGCCGTTTTTTCGGCGAGCGGCGTGTCATTCTCATCAAGCAT      246
      |...|..|.|||.|||||||.|||.||....|..||..|.|||.||...
B_cereus    194 cacgtacacttccttttttcggagaacgtaaagtgttattaataaaaatca      243

SEQ_177     247 CCATATTTTTTTACGTCTCAAAAAGAGAAGGAGATCGAACATGATTGGC      296
      |||...|||||.|||.||..|||||||.||   |||.|||||.|||.||...
B_cereus    244 ccactctttttaacttcacaaaaagaaa---agttagaacaaaatataaa      290

SEQ_177     297 GAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCT      346
      .|...|.|||.||..||..||..||..||..||..||..||..||..|.
B_cereus    291 aattttagaagaatatattgggggaaccttctcccttttctattcttgttt      340

SEQ_177     347 TTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCTC      396
      |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||
B_cereus    341 ttgttgcgcccttacgaaaagctggatgaacgaaaaaaaattacaaaact-      389

SEQ_177     397 GCCAAAGAGCAAAGC-GAAGTCGTCATCGC---CGCCCCGCTCGCCGAAG      442
      ...|||||.|||.|||.|||.||..||   .||...||..||..|.
B_cereus    390 attaaagaaaacagcggatgtagtagaagcgaatgcaatgcaagtgcagg      439

SEQ_177     443 CGGAGCTG-CGTGCCTGGGTG--CGGCGCCGCATCGAGAGCCAAGGGGCG      489
      ..|..|.|||.||..|||   ||| |||.||..||..|||.|||.
B_cereus    440 atgttcagaagtggattgttgctcgg-gcag-atgaagtgc--atgtgca      485
```

SEQ_177	490	CA---AGCAAGCGACGAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGAC	536
B_cereus	486	tattgatcatgc-----ggctgttagtttggttagagcttg-tgggaa	529
SEQ_177	537	GCAGCTTTCCGCC--TTGGCGAATGAAATCGATAAATTGGCCCTGTTTGCC	585
B_cereus	530	gtaatgtaacgatgttggcgaaggaaatggacaagttaacgttatatgtc	579
SEQ_177	586	GGATCGGGCGGA-----ACCATCGAGGCGGCGCGGTTGAGCGGCTTGTC	630
B_cereus	580	ggtatggcgagatattacaccgaaac---tc-gttgcagagcttgt-	623
SEQ_177	631	GCCCGCACGCG--GAAGAAAACGTATTTGTGC-TTGTG-GAGCAAGTGG	676
B_cereus	624	gccaaaat-cagttgaacaaaatgtgtt--tgctttgacagaaaaagtgg	670
SEQ_177	677	CGAAGCGCGACATTCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAA	726
B_cereus	671	taaaaaagatatcgcggtgcgatgcaaattttggatggattatttaacg	720
SEQ_177	727	AACAATGAAGAGCCGATCAAAATTTGGCGTTGCTCGCCGCCCATTTCCG	776
B_cereus	721	cagcaggaggaacctattaaattgcttgcgttattagtaagtcaattccg	770
SEQ_177	777	CTTGCTTCGCAAGTGAAATGGCTTGCCTC--CTTAGGCTACGGACAGGC	824
B_cereus	771	tttactgcatcaagtgaagag-ttacagcagcgt-ggttacggtcaaaa	818
SEQ_177	825	GCAAATTGCTGCGGCGC---TCAAGGTGCACCCGTTCCGCGTCAAGCTCG	871
B_cereus	819	tcaaat--c-gcgtctcatattggtgtgcatccatatcgtgtaaaattag	865
SEQ_177	872	CTCTTGCTCAAGCGGCCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATC	921
B_cereus	866	cgatgaatcaaacgaagttttctcttttgaagaattaaaaaaagtgata	915
SEQ_177	922	AACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGG-GCGGTCGAT-	969
B_cereus	916	atggaattagcggaagctgattatagtatgaaaa-cgggaaaaatggata	964
SEQ_177	970	CGCCGGTTG-GCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCCGG	1018
B_cereus	965	agaaacttggtgc--tcgagttttcttaatgcggt-----taa	1002
SEQ_177	1019	CGCAAGCGGGGCGCCACGGCCGGCGG	1044
B_cereus	1003	catatgtga	1011

#####

Program: needle
Rundate: Wed Aug 23 15:06:55 2006
Align_format: srspair
Report_file: /ebi/extserv/old-work/needle-20060823-15065418854824.output
#####

#=====

Aligned_sequences: 2
1: SEQ_177
2: B_thuringiensis
Matrix: EBLOSUM62
Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 1067
Identity: 587/1067 (55.0%)
Similarity: 587/1067 (55.0%)
Gaps: 79/1067 (7.4%)
Score: 2694.0

#=====

SEQ_177	1	ATGC-TGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTCTCCCC	49
B_thuringiens	1	atgagtgatatacata----aaaaaattaaaaagaaacagtttgctccgt	46
SEQ_177	50	TTTATTTATTATACGGCAATGAGCCGTTTTTATTAACGGAAACGTATGAG	99
B_thuringiens	47	tatatttactatatatgggacggaagccttttttataaatgaaacgataaag	96
SEQ_177	100	CGATTGGTGAAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACTTGGC	149
B_thuringiens	97	cttattacgacagaagcacttgaagaagaagatcgagagttaaat---gt	143
SEQ_177	150	TGTG---TACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGG	196
B_thuringiens	144	tgtgacatacgatttgaagaagcgtatttagaagatgtggttgaggatg	193
SEQ_177	197	C-CGAGACGGTGCCGTTTTTCGGCGAGCGGCGTGTCTATTCTCATCAAGCA	245
B_thuringiens	194	cgcgt-acgccttcctttctttggagagcggaaagtactgttaataaaatc	242
SEQ_177	246	TCCATATTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTTGG	295
B_thuringiens	243	accgctatttttgacttcgcaaaaagaaa--agttagagcaaaatataa	289
SEQ_177	296	CGAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTC	345
B_thuringiens	290	aaattttagaagaatacattgggtgaaccttctccattttctattcttgtt	339
SEQ_177	346	TTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCT	395
B_thuringiens	340	tttgttgcgcttacgaaaaacttgatgagcgaaaaaaattacaaaact	389
SEQ_177	396	CGCCAAAGAGCAAAGCGAAGTCGTCATCGCCGCCCGCTCGCCGAAGC-G	444
B_thuringiens	390	-attaaagaaaacagc--agatgtagtagaag---cgaatg-cgatgcaa	432
SEQ_177	445	GAGCTGCGTGCCTGGGTGCGGC--GCCGCATCGAG-AGCCAAGGGGCGCA	491
B_thuringiens	433	gtgcaggatgttcagaagtggattgttgc-tcgggcagatgaagtgcagt	481

SEQ_177	492	AGCA-AGCGACGAGGCGATTGATGTCCTGTTGC---GGCGGGCCGGGACG	537
B_thuringiens	482	530
SEQ_177	538	CAGCTTTCCGCC-TTGGCGAATGAAATCGATAAATTGGCCCTGTTTGCCG	586
B_thuringiens	531	580
SEQ_177	587	GATCGGGCGGAACCATCGAGGCGGCGCGGTTGAGCGGCTTGTCGCCCCG	636
B_thuringiens	581	{... 	629
SEQ_177	637	ACGCCG--GAAGAAAACGTATTGTGTC-TTGTC-GAGCAAGTGGCGAAGC	682
B_thuringiens	630	676
SEQ_177	683	GCGACATTCCAGCAGCGTTGCGACGTTTATGATCTGCTTGAAAACAAT	732
B_thuringiens	677	726
SEQ_177	733	GAAGAGCCGATCAAAATTTTGGCGTTGCTCGCCGCCCATTTCCGCTTGCT	782
B_thuringiens	727	776
SEQ_177	783	TTCGCAAGTGAAATGGCTTGC--CTCCTTAGGCTACGGACAGGCGCAAAT	830
B_thuringiens	777	824
SEQ_177	831	TGCTGCGGCGCTCAAGGTGCACCCGTTCCGCGTCAAGCTCGCTCTTGCTC	880
B_thuringiens	825	874
SEQ_177	881	AAGCGGCCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATCAACGAGCTC	930
B_thuringiens	875	924
SEQ_177	931	GCTGACGCCGATTACGAAGTGAAAAGCGGG-GCGGTGAT-CGCCGGTTG	978
B_thuringiens	925	973
SEQ_177	979	-GCCGTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCCGCGCAAGCGG	1027
B_thuringiens	974	1011
SEQ_177	1028	GGCGCCACGGCCGGCGG	1044
B_thuringiens	1012		1011

```
#####
# Program: needle
# Rundate: Wed Aug 23 15:13:23 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060823-15132265139353.output
#####

#=====
#
# Aligned_sequences: 2
# 1: SEQ_177
# 2: B_weihenstephanensis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1074
# Identity: 579/1074 (53.9%)
# Similarity: 579/1074 (53.9%)
# Gaps: 93/1074 ( 8.7%)
# Score: 2650.5
#
#
#=====

SEQ_177      1 ATGC-TGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTCTCCCC 49
               |||. ||..|..|..|..|   |||.|||||...|..|..|..|..
B_weihensteph 1 atgagtgatatacataagaag----attaaaaagaaacagttcgctccgt 46

SEQ_177      50 TTTATTTTATTATACGGCAATGAGCCGTTTTTTATTAACGGAAACGTATGAG 99
               |.|||||.|.|||.|||.|||.|||.|||.|||.|||.|||.|||.
B_weihensteph 47 tgtatgtactgtatggaacggaagcttattttataaatgaaacgataaag 96

SEQ_177      100 CGATTGGTGAACGCAGCGCTTGCCCCCGAGGAGCGGGAGTGGAACCTGGC 149
               |..|...|..|..|..|..|..|..|..|..|..|..|..|..|..
B_weihensteph 97 cttattacaacggaagcgcttgaagaggaagatcgagagttaa---gt 143

SEQ_177      150 TGTG---TACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGG 196
               ||||   |||||.|||.|||.|||.|||.|||.|||.|||.|||.
B_weihensteph 144 tgtgacatacgaatttggagaagcgctatttagaagatgtagttgaggatg 193

SEQ_177      197 CCGAGACGGTGCCTTTTTTCGGCGAGCGGCGTGTCATTCTCATCAAGCAT 246
               |..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|..
B_weihensteph 194 cgcatacgccttccttttttggagagcgtaagttatattaataaaaatca 243

SEQ_177      247 CCATATTTTTTTACGCTCTGAAAAAGAGAAGGAGATCGAACATGATTGGC 296
               |||...|||..|..|..|..|..|..|..|..|..|..|..|..|..
B_weihensteph 244 ccactatttttaacggcacaaaaagaaa---aattagaacaaaatataaa 290

SEQ_177      297 GAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCT 346
               .|...|.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
B_weihensteph 291 aattttagaagaatatattggggagccatctcctttttctattcttgttt 340

SEQ_177      347 TTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCTC 396
               |||.|||..|..|..|..|..|..|..|..|..|..|..|..|..|..
B_weihensteph 341 ttgttgcgccttatgaaaaattagacgaacgaaaaaaattacaaaact- 389

SEQ_177      397 GCCAAAGAGCAAAGCGAAGTCGTCATCGCCGCCCGCTCGCCGAAGC-GG 445
               ...|||..|..|..|..|..|..|..|..|..|..|..|..|..|..
B_weihensteph 390 attaaagaaaacagcg--gatgtaatagaag---caaatg-cgatgcaag 433

SEQ_177      446 AGCTGCGTGCCCTGGGTGCGGCGCCGCATCGAGAGC-CAAGGGGCGCAAGC 494
               .|||.||..|..|..|..|..|..|..|..|..|..|..|..|..|..
B_weihensteph 434 tgcaggatgttcagaagtgg-attgtttctcgtgaggatgaggtgcatg- 481
```

SEQ_177	495	AAGC-----GACGAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGAC	536
B_weihensteph	482	-tgcatattgataaatgcagctgttagtttattgtagagcttg-tgggaa	529
SEQ_177	537	GCAGCTTTCCGCC-TTGGCGAATGAAATCGATAAATTGGCCCTGTTTGCC	585
B_weihensteph	530	gcaatgtaacaatgttggcgaaggaaatggacaagttaacggtatacgtc	579
SEQ_177	586	GGATCGGGCGGAACCATCGAGGCGGCGGCGGTTG-AGCGG--CTTGTCGC	632
B_weihensteph	580	ggtatgggcggagaaatt---acgccaaaacttgtcacggaacttgt--g	624
SEQ_177	633	CCGCACGCCG--GAAGAAAACGTATTGTGCTTGTGCGAGCAAGTGGCGAA	680
B_weihensteph	625	cggaaatctgttgagcaaaacgtgtttgctttaacagaaaaagtggtgaa	674
SEQ_177	681	GCGCGACATTCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAAAACA	730
B_weihensteph	675	aaaagatatcgctgggtgcgatgcaaa--ttttaga-cggattatttaca	720
SEQ_177	731	---ATGAAGAGCCGATCAAAATTTTGGCGTTGCTCGCCGCCCATTTCCG	776
B_weihensteph	721	cagcaggaagaaccgattaaactgctcgctttattagtaagtcagttccg	770
SEQ_177	777	CTTGCTTTTCGCAAGTGAAATGGCTTGCCCTC--CTTAGGCTACGGACAGGC	824
B_weihensteph	771	cttgctgcatcaagtgaagag-ttgcaacagcgt-ggttacggacaaaa	818
SEQ_177	825	GCAAATTGCTGCGGCGCTCAAGGTG--CACCCGTTCCGCGTCAAGCTCGC	872
B_weihensteph	819	tcaaatcgcgtc--ccatattggtgtacatccgtaccgggtaagttggc	866
SEQ_177	873	TCTTGCTCAAGCGGCCCGCTTCGCTGACGGAGAGCTTGCTGAGGCGATCA	922
B_weihensteph	867	gatgaatcaaacgaagtttttctcttttgaagaattaaaaaaagttatta	916
SEQ_177	923	ACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGGCGGTCGAT-CG	971
B_weihensteph	917	tagaattggcgggaagctgattatagtagaagactggaaagatggataag	966
SEQ_177	972	CCGGTTG-GCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCGGCG	1020
B_weihensteph	967	aaacttgtgc--ttgagttttcttaatgcggt-----taaataca	1004
SEQ_177	1021	CAAGCGGGGCGCCACGGCCGGCGG	1044
B_weihensteph	1005	tatgtag	1011

#####

Program: needle
Rundate: Wed Aug 23 15:18:12 2006
Align_format: srspair
Report_file: /ebi/extserv/old-work/needle-20060823-15181247653341.output
#####

#=====

Aligned_sequences: 2
1: SEQ_177
2: B_subtilis
Matrix: EBLOSUM62
Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 1085
Identity: 602/1085 (55.5%)
Similarity: 602/1085 (55.5%)
Gaps: 82/1085 (7.6%)
Score: 2814.0

#=====

SEQ_177	1	ATGCTGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTC-TCCCC	49
B_subtilis	1	atggtatttgatgtgtggaaaagcc-tgaaaaaggagaggtccatccgg	49
SEQ_177	50	TTTATTTATTATACGGCAATGAGCCGTTTTTTATT-AACGGAAACGTATGA	98
B_subtilis	50	tttattgtttatacggaaaagagacatatctgctgcaagaaaccgtcagc	99
SEQ_177	99	GCGATTGGTGA-ACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACTTG	147
B_subtilis	100	aggatcagacagacg-gtcg-ttgatcaggagacaaaggatttcaatctg	147
SEQ_177	148	GCTGTGTACGA-CTG--CGAGGAAACGCC-GATCGAGGCGGCGCTTGAGG	193
B_subtilis	148	tccgtttttgatctggaagaggaccgctggatcaa---gcgattgcag	193
SEQ_177	194	AGGCCGAGACGGTGCCGTTTTTCGGCGAGCGGCG---TGTCATTCTCATC	240
B_subtilis	194	atgctgaaacgtttccgtttatgggggagcggcgtcttgtcatt---gtg	240
SEQ_177	241	AAGCATCCATATTTTTTTTACGTCTGAAAAAGAGAAGG--AGATCGAACA	287
B_subtilis	241	aaaaatccatattttttaacaggtgaaaagaaaaaagaaaaaattgagca	290
SEQ_177	288	TGATTGGCGAAGCTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTCGA	337
B_subtilis	291	caacgtcagtgcgcttgaatcatatatacaatcacctgcgccttacacag	340
SEQ_177	338	TCGTCGTCTTTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATT	387
B_subtilis	341	tctttgtcctgcttgctccgtatgaaaagcttgatgagcgaaaaaagctg	390
SEQ_177	388	AC-----GAAGCTCGC--CAAAGAGCAAAGCGAAGTCGTCATC	423
B_subtilis	391	acgaaagcgttaaagaagcacgcgtttatgatggaggcgaag--gaatta	438
SEQ_177	424	GCCGCCCCG--CTCGCCGAAGCGGAGCTGCGTGCCTGGGTGCGGCGCCGC	471
B_subtilis	439	aatgcaaaggaaacgac-agactttactgtcaacct---tgcaaaaacag	484

SEQ_177	472	ATCGAGAGCCAAAGGGCGCAAGCAAGCGACGAGGCGATTGATGTCCTG-T	520
B_subtilis	485	agcagaaaaacaatcggcac--ggaagcggcggagcatttg--gttctgct	530
SEQ_177	521	TGCGGCGGGGCCGGGACGCAGCTTTC--CGCCTTGCGGAATGAAATCGATA	568
B_subtilis	531	tgt---gaacgg--tcacatgtcatcgatttttcaggag-attcaaaa	572
SEQ_177	569	AATTGGCCCTGTTTGCCG--GATCGGGCGGAACCATCGAGGCGGCGGCGG	616
B_subtilis	573	gctctgcac-gtttattggagatcgtgaagaaattacgc--tgatgatg	619
SEQ_177	617	TTGAGCGGCTTGTCGCCCGCACGCC--GGAAGAAAACGTATTTGTGCTTGT	665
B_subtilis	620	taaaaatgcttggtgctag-aagccttgaacaaaatatttttgagctgat	668
SEQ_177	666	CGAGCAAGTGCGGAAGCGGCACATTCCAGCAGCGT-TGCAGACGTTTAT	714
B_subtilis	669	caataaaatcgtcaaccgaaaaacgaacag-agagtctgcaaatttttat	717
SEQ_177	715	GATCTGCTTGAAAACAATGAAGAGCCGATCAAAATTTTGCGCTTGCTCGC	764
B_subtilis	718	gatttgctaaaaacaaatgaagaaccgatcaaaattatggcgcttatttc	767
SEQ_177	765	CGCCCATTTCCGCTTGCTTTCGCAAGTGAAATGGCTTGCTCCTTAGGCT	814
B_subtilis	768	gaatcagttccggctgattctgcagacgaagtacttcgcggaacagggat	817
SEQ_177	815	ACGGACAGGCGCAAATTGCTGCGGCGCTCAAGGTGCACCCGTTCCGCGTC	864
B_subtilis	818	acggacaaaaacaaatcgcttctaatctaaagttcacccatttcgggta	867
SEQ_177	865	AAGCTCGCTCTTGCTCAAGCGGCCGCTTCGCTGACGGAGAGCT-TGCTG	913
B_subtilis	868	aagctggcgatggatcaagcaaggcttttttcagaggaggagctccggtt	917
SEQ_177	914	AGGCGATCAACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGG--	960
B_subtilis	918	aattattgaac-agcttgccgtcatggactatgagatgaaaaccgggaaa	966
SEQ_177	961	GCGGTCGATCGCCGTTGGCCGTTGAGCTGCTTCTGATGC-GCTGGGGCG	1009
B_subtilis	967	aaggacaagcagctcctgctc--gaactgttccttttacagctgttaaa	1013
SEQ_177	1010	CCCGCCCGGCGCAAGCGGGGCGCCACGGCCGGCGG 1044	
B_subtilis	1014	aagaaatgaaaaaac-gatccccattattga 1044	

#####

Program: needle
Rundate: Wed Aug 23 15:23:37 2006
Align_format: srspair
Report_file: /ebi/extserv/old-work/needle-20060823-15233673591570.output
#####

#=====

Aligned_sequences: 2
1: SEQ_177
2: B_licheniformis
Matrix: EBLOSUM62
Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 1123
Identity: 616/1123 (54.9%)
Similarity: 616/1123 (54.9%)
Gaps: 137/1123 (12.2%)
Score: 2964.5

#=====

SEQ_177	1	ATGCTGG-AACG-----CGTATGGGGAAACAT	26
B_licheniform	1	atgaaagaggggaaagtgcagatgacggtatttgatggttgaaaagc-t	49
SEQ_177	27	TGAAAAACGGCGTTTTTC-TCCCTTTATTTATATACGGCAATGAGCCG	75
B_licheniform	50	tgaaaaaaggcgacattcatcccgtttattgcttgtagcggaagagacg	99
SEQ_177	76	TTTTTATTAACGGAACGTATGAGCGATTGGTGAACGAGCGCTTGGCCC	125
B_licheniform	100	catcttctgcaggagacggttcaaaggatcagacaagccgttggtgatga	149
SEQ_177	126	CGAGGAGCGGGAGTGGAACTTGGCTGTGTACGA-CTGCGAGGAAACGC--	172
B_licheniform	150	agagacgaaagactttaacttctcgatatttgatctggaagaagacgcgc	199
SEQ_177	173	-CGATCGAGGCGGCGCTTGAGGAGGCCGAGACGGTGCCGTTTTTCGGCGA	221
B_licheniform	200	tcgatcttgccg---tggaggatgcggaacctttccgtttatggggga	245
SEQ_177	222	GCGGCG--TGTCATTCTCATCAAGCATCCATATTTTTTTACGTCTGAAA	268
B_licheniform	246	aaggcgtcttgctgtg-gcgaaaaac--ccggcgtttttaacagctgaaa	292
SEQ_177	269	AAGAGAAGG--AGATCGAACATGAT-TTGGCGAAGCTGGAGGCGTACTT	314
B_licheniform	293	aaaagaaggataagcttgagcataatctcggtgta-ctggaagcttacat	341
SEQ_177	315	GAAGGCGCGCTCGCCGTTTTTCGATCGTCGTCCTTTTTTCGCGCCGTACGAGA	364
B_licheniform	342	tacgcagccggcaccttattccggtgtttgtttgcttgcccttatgaaa	391
SEQ_177	365	AGCTTGATGAGCGAAAAAAATTACGAAGCTCGCCAAAGAGCA-----	407
B_licheniform	392	agctcgatgaacggaaaaagctgaccaagctcctgaaaaagcatgcccac	441
SEQ_177	408	-----AAGCGAAGTCGTCATCGCCGCC-----CCGCTCGCCGAAGC	443
B_licheniform	442	atggtggaagcgaag--gaattaaccgccaaagaaacggctgactttatc	489

SEQ_177	444	GGAGCTGCGTGCCTGGGTGCGGCGCCGCATCGAGAGCCAAGGGGCGCAAG	493
B_licheniform	490	-----gcaggcct-----cgcgaagtcggaaggcaaacaaatcgaa	525
SEQ_177	494	C---AAGCGAC-GAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGACGCA	539
B_licheniform	526	ccggaagcggcggaggagct---tgtcctgttatgtcatgcaag-----	566
SEQ_177	540	GCTTTCCGCCTTGGCGAATGAAATCGATAAATTGGCCCTG---T'TTGCC	585
B_licheniform	567	tctgtcagccattgccagga---ggttaaaaagctcagtcacatatacc	612
SEQ_177	586	GGATCGGGCGGAACCATCGAGGCGGCGCGGTTGAGCGGCTTGTGCGCCG	635
B_licheniform	613	ggtgaccgcggagagatcaccatagaggatgtcagaaagcttgtagcgag	662
SEQ_177	636	CACGCCGGAAGAAAACGTATTTGTGCTTGTGCGAGCAAGTGGCGAAGCGCG	685
B_licheniform	663	agggccttgaacaaaaatatttcgaactgatcaataaggctcgtcaatcgga	712
SEQ_177	686	ACATTCCAGCAGCGTTGCAGACGTTTTATGATCTGCTTGAAAACAATGAA	735
B_licheniform	713	aacgtacagaagcgtcgcagattttctacgatctattaaagcaaaatgaa	762
SEQ_177	736	GAGCCGATCAAAATTTTGGCGTTGCTCGCCGCCCATTTCCGCTTGCTTTC	785
B_licheniform	763	gagccgattaaaaatgatggcgctgattgctaatacagttcaggctgctgat	812
SEQ_177	786	GCAAGTGAAATGGCTTGCCCTCCTTAGGCTACGGACAGGCGCAAATGCTG	835
B_licheniform	813	gcagaccaaataattttctgaccagggatacggacaaaagcaaatcgct	862
SEQ_177	836	CGGCGCTCAAGGTGCACCCGTTCCGCGTCAAGCTCGCTCTTGCTCAAGCG	885
B_licheniform	863	caaaccttaaagtgcacccgttcagggtgaagctggcgatcgagcaggcg	912
SEQ_177	886	GCCCGCTTCGCTGA-CGGAGAGCTTGCTGAGGCG-ATCAACGAGCTCGCT	933
B_licheniform	913	aggcttttttcagagcag-gagctt---aggaacattatcgagc-agct	956
SEQ_177	934	GACGCC-----GATTACGAAGTGAA---AAGCGGGGCGGTCGATCGCCG	974
B_licheniform	957	--cgccgtgatggattatgaaatgaagacaggcaaaaaagacaa--gcag	1002
SEQ_177	975	GTTGGCCG--TTGAGCTGCTTCTGATG-CGCTGSGGGCGCCCGCCGGCGC	1021
B_licheniform	1003	ct---cctgcttgaactgttttctgctgaagctgctgcagcctcatgaaaa	1049
SEQ_177	1022	AAGCGGGGCGCCACGGCCGGCGG	1044
B_licheniform	1050	aaac-ggcctcctttaa	1065

#####

Program: needle
Rundate: Wed Aug 23 15:29:49 2006
Align_format: srspair
Report_file: /ebi/extserv/old-work/needle-20060823-15294971407139.output
#####

#=====

Aligned_sequences: 2
1: SEQ_177
2: B_halodurans
Matrix: EBLOSUM62
Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 1096
Identity: 571/1096 (52.1%)
Similarity: 571/1096 (52.1%)
Gaps: 119/1096 (10.9%)
Score: 2648.0

#=====

SEQ_177	1	ATG--CTGGAACGCGTATGGGGAAACATTGAAAAACGG--CGTTTTCCTC	46
		
B_halodurans	1	atgaactattttaaaat-taaagcaagatgtccaagcgggacgagtggccc	49
SEQ_177	47	CCCTTTATTATTATTATACGGCAATGAGCCGTTTATT-AACGGAAACGTA	95
		
B_halodurans	50	ctgtatattttatgtatgggaccgagttgtttttaatggaagacctcata	99
SEQ_177	96	-TGAGCGATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAAAC	144
		
B_halodurans	100	caggacatatt-tgtccgtaacg-ttatc-----ggatgaggaaagggat	141
SEQ_177	145	TTGGCTGTGTACGACTGC-----GAGGAAACGCCGATCGAGGCGGCGC	187
		
B_halodurans	142	atgaatgt-ttcactcttattcccttactgatgttcgattgaggcggcgc	190
SEQ_177	188	TTGAGGAGGCCGAGACGGTGCCGTTTTCGGCGAGCGCGGTGTCATTCTC	237
		
B_halodurans	191	tcgaagaagcagaaacggttccttttttggctcgaagcgggtcgtgatc	240
SEQ_177	238	ATCAA---GCATCCATATTTTTTTACGTCTGAAAAAGAGAAGGAGATCG	283
		
B_halodurans	241	ttaaaagatgctgcctattt-----acaagccaaaagcttgatgttg	283
SEQ_177	284	AACATGATTGGCGAAGCTGGAGGCGTAC---TTGAA---GGCGCCGTCG	327
		
B_halodurans	284	agcacgatgtgaaacgattggagcaatacatattgaacccagttccagag	333
SEQ_177	328	CCGTTTTTCGATCGTCTCTTTTTTCGCGCGGTACGAGAAGCTTGATGAGCG	377
		
B_halodurans	334	acggttttgctgatc-----atggcccttatgaaaagctcgatgaacg	377
SEQ_177	378	AAAAAAATTACGAAGCTCGCCAAAGAGCAAAGCGAAG-TCGTCATCGCC	426
		
B_halodurans	378	aaaaaaaatcacgaagcttatcaaa----aaagagtcgcttgcttcttgag	423
SEQ_177	427	GCC---CCGCTCGCCGAAGCGGAGCTGCGTGCCTGGGTG-CGGCGCCGCA	472
		
B_halodurans	424	gcaaagcctttggacgaaggagaggcaaaagcatggctatcctcactggc	473

SEQ_177	473	TCGAGAGC--CAAGGGGCG-----CAAGCAAGCGA-CGAGGCCGATTGATG	514
B_halodurans	474	aagcgagcttcaggtggagatggacgagaaagctatcgagacgt-----	517
SEQ_177	515	TCCTGTTGCGGCGGGCCGGGACGCAGCTT-TCGCCCTTGGCGAATGAAAT	563
B_halodurans	518	---tggtt-agggatgacgggtcttcgcttgacccaattagcatctgaaat	563
SEQ_177	564	CGATAAATTGGCCCTGTTTGCCGGATCGGGCGGAACCATCGAGGCGGCGG	613
B_halodurans	564	gaataaattagcgttgatgtagggggaaggaggcatcatccgatcagagg	613
SEQ_177	614	CGGTTGAGCGGCTTGTCGCCCCGACGCCGGAAGAAAACGTATTTGTGCTT	663
B_halodurans	614	acgtaaccttgctcgttgctaaaacgctcgatcaaacatatattgatctg	663
SEQ_177	664	GTCGAGCAAGTGGCGAAGCGCGACATTC-----CAGC-AGCGTTGCA	704
B_halodurans	664	attg--attttgc-----catcaatcagaggactcatcaagcgct-ct	703
SEQ_177	705	GACGTTT-TATGATCTGCTTGAAAACAATGAAGAGCCGATCAAAATTTTG	753
B_halodurans	704	ctctttaccatgagctcctgaaacaaaagaggagccattgaagctggtg	753
SEQ_177	754	GCGTTGCTCGC-CGCCCATTTCGCTTGCTTTCGCAAGTGAATGGCTTG	802
B_halodurans	754	gccttattaacacgpcagttt-cgcatcatgtaccaagtcaaagagcttg	802
SEQ_177	803	CCTCCTTAGGCTACGGACAGGCGCAAATTGCTGCGGCGCTCAAGGTGCAC	852
B_halodurans	803	gacgaagaggatacaccccggaatcagatggcgaagccgttaaaaattcat	852
SEQ_177	853	CCGTTCCGCGTCAAGCTCGCTCTTGCTCAAGCGGCCCGCTTCGCTG----	898
B_halodurans	853	ccctatggttgccaaacttgcgggaaaaaaagcagccagcatgtcagacca	902
SEQ_177	899	ACGGAGAGCTTGCTGAGGCGATCAACGAGCTCGCTGACGCCGATTACGAA	948
B_halodurans	903	actggttatattccctaatacg--aaaaagct-gcggatacagagtttgcg	948
SEQ_177	949	GTGAAAAGCGGGGCGGTTCGATCGCCGGTTGGCCGTTGAGCTGCTTCTGAT	998
B_halodurans	949	attaaaagtggaaaggttgataaagtgtggcattagaattgttttt---	995
SEQ_177	999	GCGCTGGGGCGCCCCCGGCGCAAGCGGGGCGCCACGGCCGGCGG	1044
B_halodurans	996	-----actcacaatgggttctag-ggagagcgtaggttag	1029

```
#####
# Program: needle
# Rundate: Wed Aug 23 15:33:21 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060823-15332034285052.output
#####

#=====
#
# Aligned_sequences: 2
# 1: SEQ_177
# 2: B_clausii
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1124
# Identity: 579/1124 (51.5%)
# Similarity: 579/1124 (51.5%)
# Gaps: 181/1124 (16.1%)
# Score: 2671.5
#
#
#=====

SEQ_177      1  ATGCTGGAACGCGTATGGGGAAACATTGAAAAACG-GCGTTTTTCTCC      47
               ..|{|...|...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii    1  atgagcatcattacggaaatgaagcaattgtcgagtgaagacaatggcacc      50

SEQ_177      48 CCTTTATTTATTATACGGCAATGAGCCGTTTTTATTAACGGAACGTATG      97
               ..|{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii    51  ggtatactttttgtatgggacaga-acgttatt-taatcgagcaattttt      98

SEQ_177      98  AGCGATTGGTGAACGCAGCGCTTGGCCCCGAGGA-----GCGGGAGTG--      140
               |{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii    99  a-caaaaagcaagcgaagcattatttgcaggggaagaaggc-gaaatgaa      146

SEQ_177     141  -GAACTTGGCTGTGTACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTT      189
               ||...|||...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii   147  tgatatctcgct---tacgcttac-aagatacgcgctaggggaagtgggtg      192

SEQ_177     190  GAGGAGGCCGAGACGGTGCCGTTTTTCGGCGAGCGG---CGTGTCAATTCT      236
               |||||..|{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii   193  gaggaagcggagactgttccgtttttctcaaagcggaaacttgttgtgat      242

SEQ_177     237  CATCAAGCATCCATATTTTTTTACGT--CTGAAA-AAGAGAAGGAGATCG      283
               |{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii   243  c--caagact-tttatttggcaacgagccagaaagtagcgacaaaaactgg      289

SEQ_177     284  AACATGATTTGGCGAAGCTGGAGGCGTA-CTGAAGGCGCCGTCGC-CGT      331
               |{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii   290  agcatgacattcccgcactggaagcctatctcgac-tcgctgcacaaga      338

SEQ_177     332  TTTCGATCGTCTCTTTTTCGCGCCGTACGAGAAGCTTGATGAGCGAAAA      381
               ...||..|{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii   339  aaccgtgc-ttgtcgttgtcgcgccgtatgaaaaattagatgaacgcaag      387

SEQ_177     382  AAAATTACGAAGCTCGCCAAAGAGCAAAGCGAAGTCGTCATCGCCG---C      428
               |||||..|{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii   388  aaaatcaccaaaaaaattaaaaaaacaaa-cgag--cgctattgatgtgaa      434

SEQ_177     429  CCCGCTCGCCGAAGCGGAGC---TGCGTGCCTGGGTGCGGCGCCGCATC      474
               .||..|{|...|{|...|{|...|{|...|{|...|{|...|{|...|{|
B_clausii   435  tccatttgatgaaaaggaaacatttgcgtggatggaggcgatagctaaac      484
```

SEQ_177	475	--GAGAGCCAAGGGGCG--CAAGCAAGCGACGAGGCGATTGATGTCTCTGT	520
B_clausii	485	aggagggc---gttgcgattcgagcaagacgcgaagcaattgctgtat--a	529
SEQ_177	521	TGCG-GCGGGCCGGGAC--GCAGCT-TTCCGCC-----TTGGCGAA-TGA	560
B_clausii	530	agcgtacaggccctaacttgatgtgtgttgccacgtgaattggagaagtgc	579
SEQ_177	561	A-----ATCGATAAATTGG---CCCTGT--TTGCCGGATCGGGCG--GA	597
B_clausii	580	atggtgtatagcaaagacggggacccagtcacagcaagcattgtcgacga	629
SEQ_177	598	ACCATCGAGGCGGCGCGGTTGAGCGGC-----TTGTGCCCCG	635
B_clausii	630	ac--tcgttgctgagacagtggaaacaaagtgtatttactgttattgacta	677
SEQ_177	636	CACGCCGGAAGAAAAAGTATTTGTGCTTGTGCGAGCAAGTGGCGAAGCGCG	685
B_clausii	678	cacggcgaaag-----gc---cgtgctggtgacgcggtccg	710
SEQ_177	686	ACATT-CCAGCAGC-GTTGCAGACGTTTTATGATCTGCTTGAACAATG	733
B_clausii	711	gctttaccaccagctgttg-aggc-----aaaaag	739
SEQ_177	734	AAGAGCCGATCAAAATTTTGGCGTTGCTCGCCGC--CCATTTCCGCTTGC	781
B_clausii	740	aagagccgctggccatactggcggtg-ttgacgcggcaatttcggcaatt	788
SEQ_177	782	TTTCGCAAGTGAAA---TGGCTTGCCTCCTTAGGCTACGGACAGGCGCAA	828
B_clausii	789	tttc-caggtgaaaacgaggctag---ccaaagggtacacgcaaaaagag	834
SEQ_177	829	ATTGCTGCGGCGCTCAAGGTGCACCCGTTCCGCGTCAAGCTCGCTCTTGC	878
B_clausii	835	atggcatcacagcttaaatgcatccttatgtagtaaagctcgc-catgc	883
SEQ_177	879	TCAAGCGGCCCCGCTTCGCTGACGGAGAGCTTGC---TGAGGCGATC----	921
B_clausii	884	---agcaagtcaaagcgtaaac---gaccaagcaattaagacaagctcctt	927
SEQ_177	922	AACGAGCTCGCTGACGCCGATTACGAAGTGAAAAGCGGGGC-GGTCGATC	970
B_clausii	928	atcgtttgcgaagaaactgactatgccattaaga-cagggcagggccgata	976
SEQ_177	971	GCCGGTTGGCCGTTGAGCTGCTTCTGATGCGCTGGGGCGCCCGCCGCG	1020
B_clausii	977	aagagttggcgcgctgagctgttgctgctgcgattg---gcaagcacgtaa	1023
SEQ_177	1021	CAAGCGGGGCGCCACGGCCGGCGG	1044
B_clausii	1024		1023

Exhibit 3

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ_178 348 aa

Sequence 2: G_kaustophilus 348 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99

Guide tree file created: [/ebi/extserv/clustalw-

work/interactive/clustalw-20060823-05445443.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:7434

Alignment Score 2093

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-05445443.aln]

```

SEQ_178          MLERVWGNIEKRRFSPLYLLYGNEPFLLTETYERLVNAALGPEEREWNLAVYDCEETPIE 60
G_kaustophilus  MLERVWGNIEKRRFSLLYLLYGNEPFLLTETYERLVNAALGPEEREWNLAVYDCEETPVE 60
*****:

SEQ_178          AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
G_kaustophilus  AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
*****

SEQ_178          EKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
G_kaustophilus  EKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
*****

SEQ_178          LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAALQTFYDL 240
G_kaustophilus  LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAALQTFYDL 240
*****

SEQ_178          LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVVKLALAQAAAFAD 300
G_kaustophilus  LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVVKLALAQAAAFAD 300
*****

SEQ_178          GELAEAINELADADYEVKSGAVDRRLAVEALLMRWGARPAQAGRHRGRR 348
G_kaustophilus  GELAEAINELADADYEVKSGAVDRRLAVEALLMRWGTRPAQAGRHRGRR 348
*****:*****

```



```

Sequence format is Pearson
Sequence 1: SEQ_178                                348 aa
Sequence 2: Bacillus_sp_NRRL_B14911                346 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 51
Guide tree      file created:  [/ebi/extserv/clustalw-
work/interactive/clustalw-20060823-05514556.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences:  2          Score:5730
Alignment Score 1092
CLUSTAL-Alignment file created  [/ebi/extserv/clustalw-work/interactive/clustalw-
20060823-05514556.aln]

```

[illegible]

```
SEQ_178                                VYDCEETPIEAALEEAETVPFFGERRVILIKHPYFFTSEKEK-EIEHDLA 99
Bacillus_sp_NRRL_B14911              TYDLEETPIEAALEDAETFPMFGDKRLIFLHNPSFLTSEKTGKTEHNLA 100
      ** *****:***:**::*::::* *:**** * :**:**
```

```

SEQ_178                                KLEAYLKAPSPFSIVVFFAPYEKLDERKKITKLAKEQSEVVIAAPLAEAE 149
Bacillus_sp_NRRL_B14911              KLESYLKEPSPYSIIVFAAPYEKLD DRKKITKELKKKASVLEAKKLGEQE 150
***:*** ***:***:*** *****:***** *:::*: * *.* *

```

```
SEQ_178          LRAWVRRRIESQGAQASDEAIDVLLRRAGTQLSALANEIDKLALFAGSGG 199
Bacillus_sp_NRRL_B14911 LKVWIRERAAQNGVQIEEDAVQLMLTLAGTNLFMLTGGEIDKLALYADEEK 200
*.***.*..**.*.....*   ***:* *:.*****:*
```

```
SEQ_178 TIEAAAVERLVARTPEENVFVLVEQVAKRDI PAALQTIFYDLLENNEEPIK 249  
Bacillus_sp_NRRL_B14911 LIDAEAVDKLVARSLQNIFTLVDKVVRHKKIDEALRIYYDLLKQNEEPIK 250
```

: *:***** :*:~::~****:

```

SEQ_178                                TLALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFA 299
Bacillus_sp_NRRL_B14911              ILSILTGQFRLIYQVKELSRRGYGQQQTAGYLKVHPPFRVKLAAGQAQLFG 300
***::*:~***: *** *: ***** * *.***** ** *
```

```

SEQ_178                               DGELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHGRR 348
Bacillus_sp_NRRL_B14911             DEELSRIMKLLAEADYEMKTGGMNKEMLIEMFLFRLHDHALHKQTK--- 346
* * * * * : * * * * * : * * * * * : * * * * * : * * * * * :

```

Sequence format is Pearson

Sequence 2: B cereus cytotoxis 336 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 46

```
Guide tree      file created:    [/ebi/extserv/clustalw-
```

```
work/interactive/clustalw-20060823-06030715.dnd]
```

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5437

Alignment Score 961

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-06030715.aln]

```
SEQ_178          MLERVWGNIEKRRFSPYLLLYGNEPELLTETIERLVNAALGPEEREWNLAVYDCEETPIE 60  
B_cereus_cytotoxis -MSDIHKKIKKQFAPFYLLYGTEAYFINETIDLITVEALAEEDRDFNIVTYDLEEAYLE 59  
      . : * : * : * : * : * : * : * : * : * : * : * : * : * : *
```

```

SEQ_178      AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
B_cereus_cytotoxis DVVEDARTLPFFGERKILLIKSPLFLTSQKEK-LEQNIKILEEYIAEFPSPFSIMIFIAPY 118
      .*:.*:*****:***** * *:***:*** :*:*** ** *: *****:***:***

```

```

SEQ_178      EKLDERKKITKLAKSEQSEVVIAAPLAEAE LRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
B_cereus__cytotoxis  EKLDERKKITKLLKKTAEVVEANAMQVQDVRKWIVKRAEEVHVHVEEA VSLLELVGSN 178
***** * : : * : : * : : * : : * : : * : : * : :

```

```

SEQ_178          LLSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAAALQTFYDL 240
B_cereus_cytotoxis VTMLAKEMDKLTLVVGTTGGDITTKLVSELVPKSVEQNVFALTEKVVKKDIAGAMKILDGL 238
:: **::*****::***** * : * . ** :: *****::*****::*****::*

```

```

SEQ_178          LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAAQAAARFAD 300
B_cereus_cytotoxis  FTQQEPIKLLALLVSQFRLLHQVKELQQRGYGQNQIASHIGVHPYRVKLANQTKLFSF 298
: : :*****:*****:***** ** * . **** *: : ****:*****: * : * :

```

```

SEQ_178          GELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHRGR 348
B_cereus_cytotoxis EELKKVIFELAEADYSMKTGKMDKKLVLEFFLMRLNHN----- 336
      * * * * * : * * : * * : * * : * * :

```

Sequence format is Pearson

Sequence 2: B anthracis 336 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 47

```

Sequence (112) alignment done:
Guide tree      file created: [/ebi/extserv/clustalw-

```

work/interactive/clustalw-20060823-14525436.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5427

Alignment Score 958

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-

20060823-14525436.aln]

B anthracis -MSDIHKKIKKKQFAPLYLLYGTEAFFINETIKLITTEALEEEDREFNVVTYDLEEAYLE 59

之

：， ： * * * * * ， * * : * * * * * , * * * * *

B anthracis DVVEDARTLPFFGERKVLLIKSPLFLTSQKEK-LEQNIKILEEYIGEPSFSPFSILV FVAPY 118

. * * * * *

B anthracis EKLDERKKITKLLKKTADIVEANAMQVQDVQKWIVARAEEGHVHIDNAAVSLLELVGSN 178

* * * * *

B anthracis VTMLAKEMDKLTLYVGMGGEITPKLVAELVPKSVEQNVFALTEKVVKKDIAGAMQILDGL 238

[illegible]

B anthracis FTQQEPIKLLALLVSQFRLHQQVKELQQRGYGQNQIASHIGVHPYRVKLANMQTKFFSF 298

: : * * * * * : * * * * : : * * * * * * * * : : * * * : * * * * * : * : * :

B anthracis EELKKVIIELAEADYSMKTGKMDKKLVLEFFLMRLNHM----- 336

*** : * ** * : * * * : * : * : * : * : * * *

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ_178 348 aa

Sequence 2: B_cereus 336 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 47

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-14582093.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5422

Alignment Score 953

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-14582093.aln]

```

SEQ_178      MLERVWGNIEKRRFSPPLYLLYGNEPFLLTETTYERLVNAALGPEEREWNNAVYDCEETPIE 60
B_cereus     -MSDIHKKIKKKQFAPLYLLYGTEAFFINETIKLITTEALEEEDREFNVVTYDLEEAYLE 59
              :. :  :*::*:*****.**::** : ... ** *::*:**.** :*:

SEQ_178      AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
B_cereus     DVVEDARTLPFFGERKVLLIKSPLFLTSQKEK-LEQNIKILEEYIGEPSPFSILVVFVAPY 118
              .:*:**.*:*****:***** * *::*:** * :*:  ** * : *****:*.***

SEQ_178      EKLDERKKITKLAKSEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
B_cereus     EKLDERKKITKLLKKTADVVEANAMQVQDVQKWIVARADEVHVHIDHAASVLLLELVGSN 178
              ***** ** : :*** * . :   :*: * : . . *::** .*::

SEQ_178      LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDI PAALQTFYDL 240
B_cereus     VTMLAKEMDKLTLYVGMGGDITPKLV AELVPKSVEQNVFALTEKVVKKDIAGAMQILDGL 238
              :: **::*:*****:*. * ** * . * .**:: :*:***.*.*:*.***.*: : .*

SEQ_178      LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAAARFAD 300
B_cereus     FTQQEETPIKLLALLVSQFRLHQQVKELQQRGYGQONQIASHIGVHPYRVKLMNQTKFFSF 298
              : :*:*****:*****:***** ** * . ***** **: : ***:*****: * : *:

SEQ_178      GELAEAINELADADYEVKSGAVDRRLAVELLLMRWGARPAQAGRHRGR 348
B_cereus     EELKKVIMELAEADYSMKTGKMDKKLVLEFFLMRLNHM----- 336
              ** :.* ***:***:*** :*:**.*:*** .

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ_178 348 aa

Sequence 2: B_thuringiensis 336 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 47

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15064397.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5424

Alignment Score 955

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15064397.aln]

```

SEQ_178          MLERVWGNIEKRRFSPLYLLYGNEPFLTETTYERLVNAALGPEEREWNLAVYDCEETPIE 60
B_thuringiensis -MSDIHKKIKKKQFAPLYLLYGTEAFFINETIKLITTEALEEEDREFNVVTYDLEEAYLE 59
                  :. :  :*::*:*****.*.*::.* : :.. **  *::*:.....* ** : *

SEQ_178          AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY 120
B_thuringiensis DVVEDARTLPFFGERKVLLIKSPLFLTQSKEK-LEQNIKILEEYIGEPSFVSILVVFVAPY 118
                  .:*.:.*:*****:*.*** * *:***:*** :*:::  ** *:  *****:*.***

SEQ_178          EKLDERKKITKLAKSEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ 180
B_thuringiensis EKLDERKKITKLLKKTADVVEANAMQVQDVQKWIVARADEVHVHIDNAAVSLLELVGSN 178
                  ***** * : :.* * . : : : * : * :. . : : *::*. .*:

SEQ_178          LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDI PAALQTFYDL 240
B_thuringiensis VTMLAKEMDKLTLYVGMGGEITTKLVAELVPKSVEQNVFALTEKVVKKDIAGAMQILDGL 238
                  : : *::*:***:*.:. * ** * : * .**.: : *::*.:.*:.*:.*:.*:.*:.* : .*

SEQ_178          LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAAQAAAFAD 300
B_thuringiensis FTQQEEPIKLLALLVSQFRLLYQVKELQQRGYGQNQIASHIGVHPYRVKLMNQTKFFSF 298
                  : : :*****:*****.:***** *** * . **** *: : *::*:*****: * : *

SEQ_178          GELAEAINELADADYEVKSGAVDRRLAVELLLMRWGARPAQAGRHGRR 348
B_thuringiensis EELKKVIIELAEADYSMTGKMDKKLVLEFFLMRLNHM----- 336
                  ** :.* *****:***:*. :*::*.:.*:.*.

```

SEQ_178	MLERVWGNIEKRRESPLYLLLYGNEPFLLTETYERLVNAALGPEEREWNLAVYDCEETPIE	60
B_weihenstephanensis	-MSDIHKKIKKKQFAPLYVLYGTEAYFINETIKLITTEALEEEDREFNVVITYDLEEAYLE	59
	:. : :*:.*:.*:***:***.*.:.:.** : :.. ** *:*:*:..** ** : *	
SEQ_178	AALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAPY	120
B_weihenstephanensis	DVVEDAHTLPFFGERKVILIKSPLFLTAQKEK-LEQNIKILEEYIGEPSPFSILVVFAPY	118
	.:*:*.*:*****:***** * *:*:*** :*: : ** * : *****:***.***	
SEQ_178	EKLDERKKITKLAKSEQSEVVIAAPLAEELRAWVRRRIESQGAQASDEAIDVLLRRAGTQ	180
B_weihenstephanensis	EKLDERKKITKLLKKTADVIEANAMQVQDVQKWIVSRADDEVHVIDNAAVSLLELVGSN	178
	***** * : :*: * . : : : * : * :. . : : * : : ** . . : :	
SEQ_178	LSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAALQTFYDL	240
B_weihenstephanensis	VTMLAKEMDKLTLYVGMGGEITPKLVTELVPKSVEQNVFALTEKVVKDIAGAMQILDGL	238
	: : **:*:*:*:*:.* * * * . * .***: : *:*:*.*:*:*:*:*:* : *	
SEQ_178	LENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD	300
B_weihenstephanensis	FTQQEEPIKLALLVSQFRLRHQVKELQQRGYGQNGIASHIGVHPYRVKLMNQTKFFSF	298
	: : :*****:***.:*:*** ** * . **** ** : : ***:*****: * : *	
SEQ_178	GELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHRGR	348
B_weihenstephanensis	EELKKVILIELAEADYSMTGKMDKKLVLEFFMLRLNHM-----	336
	** . * ***** - * * * : * : * : * : * : * : * : *	

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ_178 348 aa

Sequence 2: B_subtilis 347 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 43

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15180145.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5401

Alignment Score 905

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15180145.aln]

```

SEQ_178      MLERVWGNIEKRRFSPPLYLLYGNEPFLLTETTYERLVNAALGPEEREWNLAVYDCEETPIE 60
B_subtilis   MVFDVWKSILKKGEVHPVYCLYGKETYLLQETVSRIRQTVDQETKDFNLSVFDLEEDPLD 60
*:  **  .:*  .. *:*  ***:.*:*  **  .*:  :*:  *  :*:*:*:  **  *::

```

```

SEQ_178      AALEEAETVPFFGERRVILIKHPYFFTSEKEKE-IEHDLAKLEAYLKAPSPFSIVVFFAP 119
B_subtilis   QAIADAETFPFMGERRLVIVKNPYFLTGEKKKEKIEHNVSALSYIQSPAPYTVFVLLAP 120
*:  :*:*.**:*:***:***:***:***:***:***:***:***:***:***:***:***:***:***

```

```

SEQ_178      YEKLDERKKITKLAKEQSEVVIAAPLAEELRAWVRRRIESQGAQASDEAIDVLLRRAGT 179
B_subtilis   YEKLDERKKLTKALKKHAFMMEAKELNAKETTDFTVNLAKEQKTIGTEAAEHLVLLVNG 180
*****:***  *:::  ::  *  *  *  :.  .  :*:  .  **  :  *:  ..

```

```

SEQ_178      QLSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAAALQTFYD 239
B_subtilis   HLSSIFQEIQKLCTFIGDREEITLDDVKMLVARSLQNI FELINKIVNRKRTESLQIFYD 240
:***:  :***:***.  *  *.  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

```

```

SEQ_178      LLENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAAQARFA 299
B_subtilis   LLKQNEEPIKIMALISNQFRLILQTKYFAEQGYGQKQIASNLKVHPFRVKLAMDAQARLFS 300
**::*****:***:  :***:  *.*:*.  *****  ***:  *****:  **  *:

```

```

SEQ_178      DGELAEAINELADADYEVKSGAVDRRLAVELLMRWGARPAQAGRHGRR 348
B_subtilis   EEELRLIIEQLAVMDYEMKTGKKDKQLLLELFLQLLKRNEKNDPHY-- 347
:  **  *:***  ***:***  *::*  :***:***:  *  :  .  *

```

```

SEQ_178      LAQAARFADGELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHGRR 348
B_licheniformis IEQARLFSEQE LRNIIEQLAVMDYEMKTGKKDKQLLLEFLKL LQPHEKNGLL--- 354
: ** *:: ** : *::** ***** *::* ::*:*** : *
```


CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ_178 348 aa

Sequence 2: B_halodurans 342 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 41

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15293846.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5263

Alignment Score 856

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15293846.aln]

```

SEQ_178      -MLERVWGNIEKRRFSPLYLLYGNEPFLLTETTYERLVNAALGPEEREWNLAVIDCEETPI 59
B_halodurans MNYLKCLKQDVQAGRVAPVYFMYGTEFLMEDLIQDILSVTLSDDEERDMNVSSYSLLTDVPI 60
              ::  :::  *.:*.:*.:*.:* *.: :  : :.:*.:*.:*.:* *.:*.:*.:*.:*

SEQ_178      EAALEEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAKLEAYLKAPSPFSIVVFFAP 119
B_halodurans EAALEEAETVPFFGSKRVVILKDAALFTSQK-LDVEHDVKRLEQYILNPVPETVLLIMAP 119
              *****.:*.:*.:*.:* *.:*.:* *.:*.:* *.:* *.:* *.:*.:*.:*

SEQ_178      YEKLDERKKITKLAKSEQSEVVIAAPLAEELRAWVRRRIESQGAQASDEAIDVLLRRAGT 179
B_halodurans YEKLDERKKITKLIKESLVLEAKPLDEGEAKAWLSSLASELQVEMDEKAIETLLGMTGL 179
              ***** *.:* *.:* *.:* *.:* *.:* *.:* *.:* *.:* *.:* *.:*

SEQ_178      QLSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAAALQTFYD 239
B_halodurans RLTQLASEMNKLALYVGEGGIIRSEDVTLLVAKTLDQNIFDLIDFAINQORTHQALSLEYHE 239
              :*: *.:*.:*.:*.:*.:* *.:* *.:* *.:* *.:* *.:* *.:* *.:* *.:*

SEQ_178      LLENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAAQAAARFA 299
B_halodurans LLKQKEEPLKLLALLTRQFRIMYQVKELGRRGYTPNQMAKPLKIHPYVAKLAGKKAASMS 299
              *.:*.:*.:*.:*.:*.:* *.:*.:* *.:* *.:* *.:* *.:* *.:* *.:*

SEQ_178      DGELAEAINELADADYEVKSGAVDRRLAVELELLMRWGARPAQAGRHGRR 348
B_halodurans DQLLYSLIEKAADTEFAIKSGKVDKVLALFLFLLTMGSRESVG----- 342
              * * . *.:* *.:*.:* *.:* *.:* *.:* *.:* *.:* *.:*

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ_178 348 aa

Sequence 2: B_clausii 340 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 37

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15331074.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:4996

Alignment Score 720

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-15331074.aln]

```

SEQ_178      -MLERVWGNIEKRRFSPLYLLYGNEPFLLTETTYERLVNAALGPEEREWNLAVIDCEETPI 59
B_clausii    MSIITEMKQLSSETMAPVYFLYGTERYLIEQFLQKASEALFAGEEGEMNDIRLRLQDTPL 60
              :      :.... :*:*:***.* :*: :  : : * :. ** * *      :***:

SEQ_178      EAALEEAETVPFFGERRVILIKHPYFFTSEKEK-EIEHDLAKLEAYLKAPSPFSIVVFFA 118
B_clausii    GEVVEEAETVPFFSKRKLVIQDFYLATSQKVATKLEHDIPALEAYLDSPAQETVLVVVA 120
              .:*****.:*:::*. . *: **:*  :***:. *****.:* :*:..*

SEQ_178      PYEKLDERKKITKLAKEQSEVVIAAPLAEAEELRAWVRRRIESQGAQASDEAIDVLLRRAG 178
B_clausii    PYEKLDERKKITKKLKKQTSVIDVNPFDKETFAWMEAIKQEGVAIEQDAKQLLYKRTG 180
              ***** *:::.. . *: * * **:.  :*: . :*: * :*:

SEQ_178      TQLSALANEIDKLALFAGSGGTIEAAVERLVARTPEENVFVLVEQVAKRDIPAALQTFY 238
B_clausii    PNLMLLHRELEKCMLYSKDGPVTASIVDELVAETVEQSVFTVIDYTAKGRAGDAVRLYH 240
              .:* * .*: * *:: .*. . *: *:.***.* *:.**.: :.* *:: :

SEQ_178      DLLENNEEPIKILALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARF 298
B_clausii    QLLRQKEEPLAILALLTRQFRQFFQVKTRLAKGYTQKEMASQLKLHPYVVKLAMQQVKAL 300
              :**.:***: *****: ** : ***  : * * * :*: **:*: *****: * . :

SEQ_178      ADGELAEAINELADADYEVKSGAVDRRLAVELLLMRWGARPAQAGRHRGRR 348
B_clausii    TTKQLRQALIVCEETDYAIKTQADKELAVELLLLRLAST----- 340
              :  * :*:  :** :*: * .:*****:* .:

```